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HNHHF52	7594	726576	AP000974	37556	1-309
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HEIAX24	8789	677177	AL136366	40612	1-134
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HEIAX24	8789	677177	AL136362	40614	1-719
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HEIAU39	8791	861503	AC011899	40619	1-535
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HELAR07	8792	953626	AC007365	40623	1-411
HEIAJ39	8793	705643	AL359186	40624	1-411
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HEIAJ39	8793	705643	AL359186	40627	1-527
HEIAJ39	8793	705643	AL139143	40628	1-2536
HEIAI86	8794	785680	AC005368	40629	1-2178
HEIAI86	8794	785680	AC008781	40630	1-215
HEIAI86	8794	785680	AC005368	40631	1-215 1-390
HELAI86	8794	785680	AC008781	40632	1-390
HEIAI86	8794	785680	AC005368	40633	1-539
HEIAI86	8794	785680	AC008781	40634	1-539
HEIAD76	8795	574163	AC023920	40635	1-339
	10,72	374103	AC023720	40033	930-987
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					4696-4886
HEIAD76	8795	574163	AC026285	40636	1-361
HEIAD76	8795	574163	U73647	40637	1-263
					856-1068
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HEIAD76	8795	574163	AC023920	40638	
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HEIAC62	8796	745672	AP001437	40643	1-426
HEIAC62	8796	745672	AP000153	40644	1-142
HEIAC62	8796	745672	AP000153	40645	1-140
HEIAC62	8796	745672	AP001437	40646	1-142
HEIAC62	8796	745672	AP001437	40647	1-140
HDTMJ27	8797	851806	AL355273	40648	1-577
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HDTMJ27	8797	851806	U82208	40649	1-123
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HDTLI05	8798	928253	AP001034	40651	1-964
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					12876-13262
1					13269-13573
					14560-14656
	1				14762-14847
					15094-15463
HDLAX52	9058	726241	AC012468	41163	1-128
HDLAW58	9059	735559	AP000634	41164	1-961
HDLAW58	9059	735559	AC015500	41165	1-961
HDLAV11	9060	852919	AL356780	41166	1-120
HDLAV11	9060	852919	AL137791	41167	1-1155
HDLAV11	9060	852919	AC023038	41168	1-1153
HDLAV11	9060	852919	AL137791	41169	1-269
HDLAV11	9060	852919	AC023038	41170	1-269
HDLAV11	9060	852919	AL137791	41171	1-114
HDLAV11	9060	852919	AC023038	41172	1-114
HDLAC67	9062	751699	AC025029	41173	1-692
HDLAC67	9062	751699	AC025029	41174	1-385
HDLAC51	9063	799888	AL359454	41175	1-131
					1985-2461
					2493-4000
HDLAC51	9063	799888	AP002766	41176	1-131
					1986-2462
					2494-4001
HDLAC30	9064	799891	AC006349	41177	1-465
HDLAC30	9064	799891	AC006349	41178	1-309
HDCBF12	9066	969401	AC069208	41179	1-544
HDCBF12	9066	969401	AC069208	41180	1-168
HDCBF12	9066	969401	AC069208	41181	1-414
HDCBD07	9067	951948	AC005955	41182	1-414
HDCBD07	9067	951948	AC005955	41183	1-428
		1555	1100005555	71103	1141-1189
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MDCAN06					- 	
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HBJDZ49	9502	847928	AC005488	42396	1-867
					1144-2852
					2949-4487
					4579-5789
					5978-9485
					10048-10911
					11334-11700
	İ				12034-12509
					13205-13321
IID ID 740	0.500	0.47000			13907-14417
HBJDZ49	9502	847928	AC005488	42397	1-735
TTD 770 57 10					738-975
HBJDZ49	9502	847928	AC005098	42398	1-866
		*			1143-2850
					2949-4489
					4581-5793
		ĺ			5905-8184
					8255-9460
			,		10026-10834
					11078-11157
					11307-11672
					i
					12131-12486
					13183-13299
HBJDZ49	9502	947029	4 000 5000	10000	13912-14426
HBJDZ49		847928	AC005098	42399	1-937
DDJDZ49	9502	847928	AC004166	42400	1-868
					1146-2858
	ļ				2957-4497
					4589-5801
İ					5913-9479
					10043-10851
		Í			11095-11174
					11333-11698
					12157-12512
					13938-14451
HBJDZ49	9502	847928	AC004166	42401	1-583
			120001100	12.01	834-1954
HBJDZ49	9502	847928	AC005071	42402	
HBJDZ49	9502	847928	AC061712	42403	1-896
112022.5	3302	047520	AC001/12	42403	1-1123
					1396-3493
					3581-3836
					3838-7040
IID ID 7740	0.500	0.47000			7048-8923
HBJDZ49	9502	847928	AC005071	42404	1-513
					2138-2341
	İ				2878-3828
	1				4039-4407
					4438-5711
					6609-6900
					6969-7501
					7547-7645
					7882-8496
					8569-9146
					9288-11595
					11642-11927
					1
					12146-12299

					
					12591-12757
				ŀ	13029-13369
					13719-14460
1		ļ			14563-14623
					14709-15271
					15352-16582
					16831-17249
					17276-17914
}				1	17947-18016
1					18327-19493
					19719-20635
					21586-21816
					24795-25126 26501-26923
					27475-28264
					28742-29110
					29565-29655
					29657-29867
					31272-31718
HBJDR24	9503	677407	AC009951	42405	1 1-642
HBJDR24	9503	677407	AC009951	42406	1-327
HBJDR24	9503	677407	AC009951	42407	1-486
					993-1122
HBJDQ86	9504	784654	AL133548	42408	1-50
					3009-3073
					4198-4253
					5692-5831
					6776-6827
					8851-8970
					9968-10050
					12598-12974
					13262-13364
					16417-16776
IIDIDOSC	0504	504654			19112-20566
HBJDQ86	9504	784654	AL133548	42409	1-1017
HBJDM70 HBJDM70	9505	757435	AC010894	42410	1-380
HBJDL24	9505 9506	757435	AC010894	42411	1-502
HBJDL24	9506	678272	AC008675	42412	1-996
HBJCQ65	9508	678272	AC008675	42413	1-300
IIDICQUI	9308	876430	AF192303	42414	1-1230
HBJCJ82	9509	779645	AT 161456	42415	1271-3810
HBJCJ82	9509	779645	AL161456 AL158075	42415	1-1118
HBJCJ82	9509	779645	AL158075	42416	1-1523
111030302	7509	779043	AL1360/3	42417	1-853
HBJCJ82	9509	779645	AL158075	42418	1340-2553
HBJCE07	9510	954090	AC025605	42418	1-482
		757090	AC023003	72417	1-357 443-919
HBJCE07	9510	954090	AC073101	42420	1-357
HBJCE07	9510	954090	AC025605	42421	1-653
HBJCE07	9510	954090	AC073101	42422	1-033
HBJCE07	9510	954090	AC073101	42423	1-420
HBJBR04	9512	847952	AC005682	42424	1-458
HBJBR04	9512	847952	AC005682	42425	1-373
HBJAP95	9513	796659	AL138715	42426	1-1044
HBJAP95	9513	796659	AL031601	42427	1-1044
				/	1338-1600
				<u> </u>	1220-1000

					2644-3247
HBJAP95	9513	796659	AL138715	42428	1-717
HBJAP95	9513	796659	AL138715	42429	1-265
HBJAP95	9513	796659	AL031601	42430	1-706
HBJAJ49	9515	723164	AC078846	42431	1-416
					1103-1882
HBJAJ49	9515	723164	AC078846	42432	1-116
HBJAH27	9517	682941	AC016325	42433	1-69
					560-632
-					2298-2395
					2510-2613
					3563-3801
					5031-5598
					5763-5801
HBJAE32	9518	699695	AC044843	42434	1-487
					983-1447
HBJAE32	9518	699695	AC008525	42435	1-487
					983-1447
HBJAE32	9518	699695	AC008525	42436	1-337
HBJAB49	9520	722195	AF276759	42437	1-1613
HBJAB49	9520	722195	AC019031	42438	1-1613
HBJAB49	9520	722195	AF276759	42439	1-561
HBJAB49	9520	722195	AC019031	42440	1-561
HBJAB28	9521	847966	AC023071	42441	1-736
HBJAB15	9522	660552	AP001931	42442	1-1266
HBJAB15	9522	660552	AP000727	42443	1-1264
HBJAB15	9522	660552	AP001931	42444	1-366
HBJAB15	9522	660552	AP001931	42445	1-308
HBJAB15	9522	660552	AP000727	42446	1-366
HBJAB15	9522	660552	AP000727	42447	1-308
HBDAE47	9523	720008	AL353776	42448	1-1591
HBDAE47	9523	720008	AL353776	42449	1-490
HBDAD16	9525	661560	AC013396	42450	1-1371
HBDAD16	9525	661560	AC013396	42451	1-296
HBDAD16	9525	661560	AC013396	42452	1-204
HBCCO10	9526	963157	AC009634	42453	1-575
HBCCO10	9526	963157	AC011721	42454	1-575
HBCCO10	9526	963157	AC009634	42455	1-206
HBCCO10	9526	963157	AC011721	42456	1-206
HBCCO10	9526	963157	AC011721	42457	1-86
HBCCJ05	9527	930956	AC068322	42458	1-600
HBCCJ05	9527	930956	AC027243	42459	1-600
HBCCJ05	9527	930956	AC024059	42460	1-600
HBCCJ05	9527	930956	AC010868	42461	1-584
HBCCJ05	9527	930956	AC068322	42462	1-364
HBCCJ05	9527	930956	AC027243	42463	1-424
HBCCJ05	9527	930956	AC068322	42464	1-450
11200000	3321	750750	AC006522	42404	1112-1585
HBCCJ05	9527	930956	AC027243	42465	1-460
	1552	750750	11002/243	72703	1112-1585
HBCCJ05	9527	930956	AC024059	42466	1-456
HBCCJ05	9527	930956	AC010868	42467	1-436
HBCCJ05	9527	930956	AC010868	42468	
HBCCD06	9529	938319	AC010808 AC007783	42469	1-335
	7527	730319	AC007703	72707	2508-3084
					3578-3890

					
					4198-4294
					4376-4623
					4712-5349
					5369-6088
					6527-7107
					7298-7392
					7730-7846
					9147-9476
				-	10487-10575 10791-11298
					11485-11601
					11783-13009
!					13207-13501
					13540-13772
					14439-14800
					14923-14983
					15133-15355
					15485-15653
					16750-16805
					16894-17078
			ļ		17162-17219
					18003-18089
					21085-21146
					21358-21501
HBCCD06	9529	938319	AC007783	42470	1-308
HBCCD06	9529	938319	AC007783	42471	1-1024
HBCCB51	9530	975256	AL139353	42472	1-71
					265-794
					1791-2077
					2409-2656
HBCBN51	9532	952057	AC073846	42473	1-141
					323-951
			ľ		1073-1625
TID CD3151	0.500		W1144		1640-2371
HBCBN51	9532	952057	AC073846	42474	1-285
HBCBF12	9535	969578	AC068735	42475	1-530
HBCBF12	9535	969578	AC021725	42476	1-534
HBCBF12	9535	969578	AL021368	42477	1-382
					762-1102
HBCBF12	0525	0.00.770	1 00 00 0	10.150	1231-1761
HBCBF12	9535 9535	969578	AC068735	42478	1-342
HBCBF12	9535	969578	AC021725	42479	1-342
HBCBF12		969578	AC068735	42480	1-659
HBCBF12	9535	969578	AC021725	42481	1-679
	9535	969578	AL021368	42482	1-664
HBCBF12	9535	969578	AL021368	42483	1-307
HBCBE57	9536	848322	AL031666	42484	1-1235
HBCBE57	9536	848322	AL031666	42485	1-508
HBCBE57	9536	848322	AL031666	42486	1-648
HBCBB22	9537	848325	AC010735	42487	1-900
HBCAT10	9539	968195	AL357521	42488	1-374
HBCAT10	9539	968195	AL021528	42489	1-374
	9539	968195	AL357521	42490	1-689
HBCAT10	9539	968195	AL357521	42491	1-355
	^				
HBCAT10	9539 9539	968195 968195	AL021528 AL021528	42492 42493	1-689 1-355

HBCAS32	9540	699489	1.0007101	10101	
IIDCA332	9340	099489	AC007101	42494	1-215
					867-1214
}					1226-2260
HBCAQ85	9541	783431	1.0010071	42405	2359-2415
IDCAQ65	9341	763431	AC019071	42495 .	1-831
					1116-1365
]]	1600-1920
					2161-2334
					2902-3156
					3364-3836
					4074-4278
					4306-4417
					4485-4581
				j	4693-4853
					4995-5264
					5758-5863
					6411-6509
HBCAQ85	9541	783431	AC019071	42496	6551-6922
HASCG58	9543	738423	AC011116	42497	1-869
HASCG58	9543	738423	AC078794	42498	1-870
HASCG58	9543	738423	AC011116	42499	1-971
HASCG58	9543	738423	AC078794	42500	1-623
HASCG58	9543	738423	AC011116	42501	1-623
HASAW90	9544	789112	AC010234	42502	1-023
HASAW90	9544	789112	AC021464	42503	1-2931
		, 0, 1,2	110021404	42303	332-547
					909-1209
					2280-2634
				1	3445-3539
					4477-4620
					7577-10496
					12087-13447
					13462-15091
					15142-16137
HASAW90	9544	789112	AC021464	42504	1-506
HASAC10	9546	968746	AC007677	42505	1-477
HASAC10	9546	968746	AC007677	42506	1-1410

[052] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEO ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

Clone ID	Contig	SEO	Analysis	PFam/NR Description	DFom/MD A	ν.		
NO:Z	Ë	NO:X	Method		Number	Score/ Percent	N.I From	
HAMHB21	961376	11	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	100	497	916
HBDAC79	935414	26	HMMER 2.1.1	PFAM: Acyl-CoA dehydrogenase	PF00441	102.6	94	342
			blastx.14	(AL021958) fadE9	gi 2911026 emb CAA	62%	94	255
	···			[Mycobacterium]	17519.1	51%	. 250	384
				tuberculosis]		64%	348	422
HRIAG72	722733	33		DEA14. 7: 1: 1:	00000	33%	0	89
7/01/01/	(7/77)	36	HIMIMER 1.8	FFAIN: Zinc-binding metalloprotease domain	PF00099	2.32	83	115
HBJGT92	919507	107	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	7.68	377	436
HBJIY20	669519	141	HMMER 2.1.1	PFAM: Orn/Lys/Arg decarboxylase	PF01276	53.1	49	162
HBMBU24	677240	234	HMMER 1.8	PFAM: Core histones H2A. H2B. H3 and H4	PF00125	7.72	139	192
HBMBZ71	880580	238	HMMER 1.8	PFAM: von Willebrand factor tyne D domain	PF00094	26.52	200	526
HBMDC16	888206	258	blastx.2	Butyrophilin-like protein BUTR-1.	sp AAF72554 AAF72 554	20%	19	315
HBMU090	928078	294	blastx.14	Zfp61p [Mus musculus]	gi 887887 gb AAC52	84%	24	119
HBMXE31	573323	317	HMMER	PFAM: Gonadotropin-	PF00446	10.78	112	141
HCFCF47	894415	372	HMMFR	DFAM: Firbarrotic anothin	DEDOOCO	1 00		
		1	1.8	kinase domain	ri.nnno3	89.54	70	295
HCFCJ21	671028	374	HMMER	PFAM: Core histones	PF00125	12.79	123	188

		1 %	HOA HOB H3 and HA				
945122	391	blastx.14	p34 protein [Rathus sn]	oi[534876]dhi[BAA02	0107	100	15
				786.1	100%	120 236	191 271
1					85%	71	91
953876	449	blastx.14	(AF079098) arginine- tRNA-protein transferase	gi 3806094 gb AAD1 2366.1	87%	5	97
			1-1p; ÅTE1-1p [Homo sapiens]				
967484	478	blastx.14	Ps 2=basic proline-rich	gi 386433 gb AAB27	37%	158	63
			protein(PRB1L precursor	289.1	53%	62	24
			l 1 [Homo sapiens]		35%	325	242
	- <u>,</u>				40%	133	59
					28%	158	63
					40%	133	59
					36%	225	160
					36%	225	160
					41%	74	24
					41%	74	24
					32%	325	242
					33%	158	87
					36%	158	93
					36%	183	118
					71%	44	24
					71%	44	24
015740					35%	74	24
912/47	248	HMMER 2.1.1	PFAM: tRNA synthetases class II (A)	PF01411	35.1	269	930
		blastx.14	ORF YNL040w	gi 1301892 emb CAA	42%	763	972
			Saccharomyces	95907.1	52%	658	759
			cerevisiae]		31%	1153	1293
					42%	1678	1740

1149	42	226	284	73	387	83	301	51	179	227	166	8 8	266	306
1009	13	173	102	2	316	235	321	13	6	202	65	316	153	262
21%	5.43	7.99	73.02	4.81	3.55	47%	71%	9.77	63%	%09 %09	85%	59%	26%	46%
	PF00196	PF00020	PF00106	PF00505	PF00018	gi 1653272 dbj BAA1 8187.1	PF01514	PF00010	gi 42759 emb CAA25		gi 1655655 emb CAB	gi 43952 emb CAA43	gi 309183 gb AAA37	443.1
	PFAM: Bacterial regulatory proteins, luxR family	PFAM: TNFR/NGFR cysteine-rich region	PFAM: Alcohol/other dehydrogenases, short chain type	PFAM: HMG (high mobility group) box	PFAM: Src homology domain 3	hypothetical protein [Synechocystis sp.]	PFAM: Secretory protein	Of YSCJ/FIIF family PFAM: Helix-loop-helix DNA-binding domain	URF (pot. 4.5S protein) [Escherichia coli]		lepA [Mycobacterium tuberculosis]	xylose isomerase [Klebsiella nneumoniae]	collagen type XVII [Mus	musculus
	HMMER 1.8	HMMER 1.8	HMMER 1.8	HMMER 1.8	HMMER 1.8	blastx.14	HMMER	HMMER 1.8	blastx.14		blastx.14	blastx.14	blastx.14	
(595	647	029	702	748	759	782	799	608		810	812	825	
1000	964857	880730	706471	615198	702435	932623	667283	968515	967717		934909	921653	924638	
OFFICE	HCUEUI0	HCUGB48	HCUGR38	HCUHM44	HCWAK80	HCWAR05	HCWBB63	HCWBE76	HCWBI37		HCWBI53	HCWBI90	HCWBN06	

46	140	303	357	360	119	287	74		264	381		167	120		198)		168		179	215	200	373	477	613		84
5	75	259	310	337	78	147	3		31	229		117	73		25			121		15	6	18	281	391	416		365
57%	36%	46%	43%	75%	42%	42%	54%		69.62	80		85%	87%		27.3		-	4.63	*****	62.98	%69	44%	51%	41%	81.59		79%
						gi 536588 emb CAA8	5172.1		PF00501	PF01991		gi 2506078 dbj BAA2	2622.1		PF00497			PF00099		PF00005	gb AAC76377.1				PF00196		gi 151190 gb AAA25
						ORF YBR208c	[Saccharomyces	cerevisiae	PFAM: AMP-binding enzymes	PFAM: ATP synthase (F/31 kDa) subunit	the standard subdime	tetracycline transporter-	like protein [Mus	musculus]	PFAM: Bacterial	extracellular solute-	binding proteins, family 3	PFAM: Zinc-binding	metalloprotease domain	PFAM: ABC transporters	(AE000411) putative	ATP-binding component	of a transport system	[Escherichia coli]	PFAM: Bacterial	regulatory proteins, luxR family	copC peptide
						blastx.14			HMMER 1.8	HMMER 2.1.1	112-4-14	olastx.14			HMMER	2.1.1		HMMER	1.8	HMMER 1.8	blastx.2				HMMER	1.8	blastx.14
-						834	· · · · · · · · · · · · · · · · · · ·		891	606	0.45	745			952			957		973					993		1014
						988026			529230	693632	027/627	754027			527555			889416		839104					974478		967361
						HCWBQ03			HCWCM65	HCWCR31	HCW/DI64	FOTO W OTT			HCWDJ23			HCWDL45	7 O 15 Can and O 1 +	HCWDR01					HCWDV17		HCWDX22

HCWDX76 932614 1019 blastx.14 HCWED61 971865 1041 blastx.14 HCWEG69 948693 1058 HMMER HCWEI19 948690 1066 HMMER HCWEL01 916972 1086 blastx.14 HCWEM51 920887 1096 blastx.14 HCWEQ14 908245 1105 HMMER HCWEW45 571355 1116 HMMER	blastx.14 (AF102543) unknown [Zymomonas mobilis] blastx.14 gp210 (AA 1-1886) [Rattus norvegicus] HMMER PFAM: Zinc-binding netalloprotease domain blastx.14 orf3 [Pseudomonas aeruginosa] HMMER PFAM: Zinc-binding 1.8 metalloprotease domain blastx.14 formaldebyde	gj 4378174 gb AAD1 9419.1	20%		000
1041 1058 1066 1086 1096 1105		9419.1	,	44	232
1041 1058 1066 1086 1096 1105			28%	6	59
1041 1058 1066 1086 1106 1116			55%	38	64
1058 1066 1086 1096 1105		gi 56463 emb CAA68 759.1	75%	481	212
1066 1086 1096 1105		PF00099	2.79	57	86
1066 1086 1096 1105		gi 557259 emb CAA5	55%	248	45
1096 1105 1116	_	PF00099	8.6	226	273
1116					
1086 1096 1105		gi 887431 emb CAA5	75%	300	10
1096 1105 1116	dehydrogenase	2057.1			-
1105	(glutathione) [Escherichia coli]				
1105	blastx.14 (AF010496) exonuclease	gi 3128267 gb AAC1	39%	34	171
1105	SbcD homolog	6119.1	47%	193	249
1105	+				
1105	Diastx.14 argininosuccinate lyase	gi[2635409[emb]CAB	54%	365	39
1116	+	14904.1	47%	57	7
1116	MMEK FFAM: DEAD and DEAH box helicases	PF00270	72.08	37	177
1116	blastx.14 (AC002985) R27090 2	gi 2443870 gb AAB8	100%	37	177
1116	[Homo sapiens]	1544.1	%99		40
1.8	HMMER PFAM: Heat shock hsp90 1.8 proteins	PF00183	10.32	37	186
954142 1125 blast	blastx.14 (AJ000758) precorrin-4	gi 3724045 emb CAA	32%	3	242
	methylase [Bacillus	04314.1)	1

181	270	152	269	236	288	09	137		158	314	211	301	393	394	112
140	34	105	105	126	214	137	9		9	195	59	310	298	341	89
4.92	36.2	4.51	71.4	50.8	4.04	73%	58.7		%98	47%	33%	41%	46%	20%	2.09
PF00018	PF00562	PF00271	PF00171	PF01197	PF00293	pir A37334 A37334	PF00165		gi 148382 gb AAA24 811.1	gi 1736771 dbj BAA1	5920.1	gi/736300 emb CAA8	8644.1		PF00130
PFAM: Src homology domain 3	PFAM: RNA polymerase beta subunit	PFAM: Helicases conserved C-terminal	PFAM: Aldehyde dehydrogenase family	PFAM: Ribosomal protein L31	PFAM: Bacterial mutT protein	L-lactate dehydrogenase (EC 1.1.1.27) - Acinetobacter 1	PFAM: Bacterial	regulatory helix-loop- helix proteins, araC family	operon regulatory protein Erwinia carotovoral	Nodulation protein V (EC	2.7.3). [Escherichia coli]	Isp42p [Saccharomyces	cerevisiae]		PFAM: Phorbol esters / diacylglycerol binding domain
HMMER 1.8	HMMER 2.1.1	HMMER 1.8	HMMER 2.1.1	HMMER 2.1.1	HMMER 1.8	blastx.14	HIMMER	1.8	blastx.14	blastx.14		blastx.14			HMMER 1.8
1143	1149	1186	1196	1217	1223	1262	1288			1295		1305			1334
506577	861907	690751	853005	861843	790796	964088	960159			889026		953384			598510
HCWFF88	HCWFK57	HCWFT29	HCWFU66	HCWGB78	HCWGE12	HCWGW12	HCWGY90			HCWHB12		HCWHD07		TOWN THE	HCWHF/4

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14	206	126	253	247	218	308	265	148	148	148	148	6	6	252	104	6	6	107	252	160	160	252	107	107	249	15	163	27
85	271	209	300	291	238	141	107	261	327	261	261	122	122	329	157	104	107	142	305	249	249	305	157	157	311	107	246	83
20%	45%	35%	43%	46%	85%	39.4	90.5	57%	45%	20%	20%	36%	34%	61%	55%	40%	33%	%99	55%	76%	76%	44%	41%	41%	33%	22%	32%	57%
gi 4584539 emb CAB	40769.1					PF00795	PF00327	gi 3510629 gb AAC8	0285.1				•			,								-				gi 1335196 emb CAA
(AL049608) extensin-like	protein Arabidopsis	thaliana]				PFAM: Carbon-nitrogen hydrolase	PFAM: Ribosomal protein L30v/L7e	(AF047828) syringomycin	synthetase [Pseudomonas	syringae pv. syringae]											•							pot. ORF I [Homo
blastx.14						HMMER 2.1.1	HMMER 2.1.1	blastx.14					•		***												+	blastx.14
1336					100,	1337	1343	1349																			_	1388
924187					0 7 0 1	5/4945	935419	924105		·· ·																	06030	886866
НС WНQ03					11011111011	нсмнүзі	HCWHR81	HCWHT59				-															UCW/I/E00	IIC WNFU8

			sapiens]	26917.1	62%	303	256
					32%	192	82
1409	\Box	blastx.14	CeoB [Burkholderia	gi 2109271 gb AAB5	55%	247	169
			cepacia]	8161.1	20%	148	83
_					62%	281	258
7,00	十				54%	61	29
1427		blastx.14	(AL121600) hypothetical	gi 6002364 emb CAB	34%	219	142
			protein SCF76.09 1	56729.1	42%	120	43
\dagger	+				57%	238	218
1437		blastx.14	ORF_0485 [Escherichia	gi 887832 gb AAA83	47%	240	7
			colij	063.1	42%	449	282
\top	۱,				35%	99	7
1442 b 	<u> </u>	blastx.14	(AF039571) peripheral	gi 4104812 gb AAD1	100%	126	263
			benzodiazepine receptor	1957.1	85%	304	345
			interacting protein; PBR-		87%	103	126
			IP/PKAX1 [Homo	-	44%	99	119
\dagger	Į.		sapiens		36%	250	315
1453 b	<u>-</u> -	blastx.14	(AC004877) sco-spondin-	gi 3638957 gb AAC3	27%	289	191
			mucin-like; similar to P98167 1 sapiens]	6301.1	71%	326	306
1462 bl	<u> </u>	blastx.14	DNA primase Escherichia colil	gi 147755 gb AAA24 600.11	45%	341	3
1470 F	1	HMMER 1.8	PFAM: E1-E2 ATPases	PF00122	55.15	2	301
	<u> </u>	blastx.2	cadmium resistance protein [Lactococcus	gb AAB37345.1	42%	2	316
1516 bl	191	blastx.14	(AE000888) malate dehydrogenase	gi 2622314 gb AAB8 5694.1	43%	66	134
			Methanobacterium		;		

	198	166	77	514	635	694	386	766	577	740	716	170	329
	151	2	33	2	537	656	811	2	335	363	513	229	48 293
	6.14	47.52	2.17	100%	51%	100%	77.2	%08	39.1	54.2	95%	50%	73%
	PF00271	PF00389 .	PF00099	gi 4405795 gb AAD1	9826.1		PF00854	gb AAD24570.1 AF1 21080_1	PF01433	PF00621	gi 5020264 gb AAD3 8043.1 AF151363_1	gi 3941737 gb AAC8	gb AAD24570.1 AF1 21080_1
thermoautotrophicum	PFAM: Helicases conserved C-terminal domain	PFAM: D-isomer specific 2-hydroxyacid dehydrogenases	PFAM: Zinc-binding metalloprotease domain	(AF038963) RNA	nelicase [Homo sapiens]		PFAM: POT family	(AF121080) cAMP inducible 1 protein [Mus musculus]	PFAM: Peptidase family M1	PFAM: RhoGEF domain	(AF151363) Cdc42 GTPase-activating protein [Mus musculus]	(AF109719) BAT2 [Mus musculus]	(AF121080) cAMP inducible 1 protein [Mus
	HMMER 1.8	HMMER 1.8	HMMER 1.8	blastx.14			HMMER 2.1.1	blastx.2	HMMER 2.1.1	HMMER 2.1.1	blastx.14	blastx.14	blastx.2
	1517	1519	1593	1633			1646		1655	1678	1694	1736	1737
	729290	654317	661570	926991			941282		947832	794275	974494	926498	741724
	HCWTR54	HCWTS15	HCWUU16	HDDMA83			HDMAQ15		HDPAG32	HDPCN94	HDPFF07	HDPIT53	HDPIT61.

340 402	280 507	152 703	127 432	4	20 76	3 734	3 734	266 313	151 387	245 376	266 451 593 673	6 59 280 351	_
4.82	39.5	54%	132.39		57%	206.63	95%	7.78	22.4	37.49	30% 48%	37%	
PF00041	PF00651	gb AAC63461.1	PF00071	emb CAA68227.1		PF00069	gi 2304746 emb CAA 03387.1	PF00036	PF00611	PF00059	gi 1323133 emb CAA 97093.1	gi 439877 gb AAB02 291.1	PF00047
PFAM: Fibronectin type III domain	PFAM: BTB/POZ domain	(AF038007) FIC1 [Homo sapiens]	PFAM: Ras family (contains ATP/GTP binding P-loop)	50	protein Homo sapiens	PFAM: Eukaryotic protein kinase domain	HUMAN NDR [unidentified]	PFAM: EF hand	PFAM: Fes/CIP4 lomology domain	PFAM: Lectin C-type domain short and long forms	ORF YGR090w [Saccharomyces cerevisiae]	nscriptase viens]	PFAM: IG
HMMER 1.8	HMMER 2.1.1	blastx.2	HMMER 1.8	blastx.2		HMMER 1.8	blastx.14	HMMER 1.8	HMMER 2.1.1	HMMER 1.8	blastx.14	blastx.14	HMMER
1750	1755	1775	1780			1788		1797	1815	1818	1837	1849	1868
959653	160606	582015	912722			934520		792193	812091	951276	919404	961323	722699
HDPKD52	HDPLC45	HDPMA48	HDPMO62			HDPNC96		HDPOJ93	HDPPP24	HDPPU44	HDPRH02	HDPSG10	HDPTW90

	518 613	412 708	349 756						3 152																
	16	81.2	36%					, 6, 0	94%	94%	94% 87% 80%	87% 80% 95%	94% 87% 95% 62%	94% 87% 80% 95% 33%	94% 87% 80% 95% 62% 33% 75%	94% 87% 80% 95% 62% 33% 75%	94% 87% 80% 95% 62% 33% 75% 37%	94% 87% 80% 95% 62% 33% 33% 37% 88%	94% 87% 80% 95% 62% 75% 75% 33% 43% 100%	94% 87% 80% 95% 62% 33% 75% 37% 43% 100% 55%	94% 87% 80% 95% 62% 33% 75% 43% 100% 55% 42%	94% 87% 80% 95% 62% 33% 75% 75% 100% 58% 43% 100% 55%	94% 87% 80% 95% 62% 33% 75% 43% 100% 55% 42% 58% 83%	94% 87% 80% 95% 62% 33% 75% 75% 43% 100% 55% 42% 58% 83%	94% 87% 80% 95% 62% 33% 75% 100% 55% 42% 55% 83% 83% 83%
	PF00169	PF00169	gb AAD04568.1					011433594119h A D1	Language	7527.1	7527.1	7527.1	7527.1	7527.1	gi[3413810 emb CAA 76598.1	gi[3413810 emb CAA 76598.1 gi[29375 emb CAA78	gi 3413810 emb CAA 76598.1 gi 29375 emb CAA78 744.1 gi 4104812 gb AAD1	gi[3413810 emb CAA 7527.1 gi[3413810 emb CAA 76598.1 gi[29375 emb CAA78 744.1 gi[4104812 gb AAD1 1957.1	gi[3413810 emb CAA 7527.1 gi[3413810 emb CAA 76598.1 gi[29375 emb CAA78 744.1 gi[4104812 gb AAD1 1957.1	gi[3413810 emb CAA 7527.1 gi[29375 emb CAA78 744.1 gi[4104812 gb AAD1 1957.1	gi[3413810 emb CAA 76598.1 gi[29375 emb CAA78 744.1 gi[4104812 gb AAD1 1957.1	gi 3413810 emb CAA 76598.1 gi 29375 emb CAA78 744.1 gi 4104812 gb AAD1 1957.1	gi[3413810 emb CAA 7527.1 gi[29375 emb CAA78 744.1 gi[4104812 gb AAD1 1957.1	gi 3413810 emb CAA 76598.1 gi 29375 emb CAA78 744.1 gi 4104812 gb AAD1 1957.1	gi 3413810 emb CAA 76598.1 gi 29375 emb CAA78 744.1 gi 4104812 gb AAD1 1957.1
superfamily	PFAM: PH (pleckstrin homology) domain	PFAM: PH domain	(AF102854) membrane-	associated guanylate	kinase-interacting protein	2 Maguin-2 [Rattus	norvegicus]	(AF061738) leucine		aminopeptidase [Homo	aminopeptidase [Homo sapiens]	aminopeptidase [Homo sapiens]	aminopeptidase [Homo sapiens]	aminopeptidase [Homo sapiens]	aminopeptidase [Homo sapiens] Bassoon [Mus musculus]	aminopeptidase [Homo sapiens] Bassoon [Mus musculus] Bat2 [Homo sapiens]	aminopeptidase [Homo sapiens] Bassoon [Mus musculus] Bat2 [Homo sapiens] (AF039571) peripheral	aminopeptidase [Homo sapiens] Bassoon [Mus musculus] Bat2 [Homo sapiens] (AF039571) peripheral benzodiazepine receptor	aminopeptidase [Homo sapiens] Bassoon [Mus musculus] Bat2 [Homo sapiens] (AF039571) peripheral benzodiazepine receptor interacting protein; PBR-	aminopeptidase [Homo sapiens] Bassoon [Mus musculus] Bat2 [Homo sapiens] (AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo	aminopeptidase [Homo sapiens] Bassoon [Mus musculus] Bat2 [Homo sapiens] (AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo sapiens]	aminopeptidase [Homo sapiens] Bassoon [Mus musculus] Bat2 [Homo sapiens] (AF039571) peripheral benzodiazepine receptor interacting protein; PBR-IP/PRAX1 [Homo sapiens]		no llus] al stor BR- ttion-	
	HMMER. 1.8	HMMER 2.1.1	blastx.2					blastx.14	•	P-14-	NAME OF THE PROPERTY OF THE PR	Market			blastx.14	blastx.14 blastx.14	blastx.14 blastx.14 blastx.14	blastx.14 blastx.14 blastx.14							
+	1877	1890						1894	_						1914	1914	1914 1936 1944	1914	1914 1936 1944	1914 1936 1944	1914 1936 1944	1914	1914	1914 1944 1945	1914 1944 1945
	96556	909916						915964							927024	927024	927024 909848	927024 909848 963481	927024 909848 963481	927024 909848 963481	927024 909848 963481	927024 909848 963481	927024	927024 909848 963481	927024 909848 963481
	HDPVG11	HDPWE80						HDPWY46							HDQEF04	HDQEF04 HDQGT70	HDQEF04 HDQGT70 HDQHT10	НDQEF04 НDQGT70 НDQHT10	HDQEF04 HDQGT70 HDQHT10	НDQEF04 НDQGT70 НDQHT10	НDQEF04 НDQGT70 НDQHT10	НDQEF04 НDQGT70 НDQHT10	HDQEF04 HDQGT70 HDQHT10	HDQEF04 HDQGT70 HDQHT10	HDQEF04 HDQGT70 HDQHT10

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352	-	. 254		255	371	403	331	347		248	356	464	297	302	170	458	509	233	354	413	326		350
65		78		79	330	371	305	159		132	273	357	163	3	3	192	492	180	244	387	108		36
42%		%86		%86	85%	100%	%99	18.53		58%	75%	58%	29.85	93.6	82%	35%	100%	7.98	78%	%88	31.58		65%
		gi 3800869 gb AAC6	0900.1	gi 3800869 gb AAC6	8900.1			PF00047		emb CAA08796.1			PF00085	PF00069	gi 1517820 gb AAC5	0918.1		PF00125	gi 919 emb CAA3980	0.1	PF00076		gb AAA35554.1
associated protein	Oryctolagus cuniculus]	(AF086624) serine	norvegicus]	(AF086624) serine	threonine kinase [Rattus	norvegicus]		PFAM: IG	(immunoglobulin) superfamily	(AJ009698) embigin	protein [Rattus	norvegicus	PFAM: Thioredoxins	PFAM: Eukaryotic protein kinase domain	p56 KKIAMRE protein	kinase [Homo sapiens]		PFAM: Core histones H2A, H2B, H3 and H4	rab4b [Canis familiaris]		PFAM: RNA recognition motif (aka RRM RRD)	or RNP domain)	arginine-rich nuclear
		blastx.14		blastx.14				HMMER	1.8	blastx			HMMER 1.8	HMMER 2.1.1	blastx.14			HMMER 1.8	blastx.14		HMMER 1.8		blastx,2
		1956		9561		,		1959	=				1968	1973				1977	1984		1987		
		973925		974565				945083					846630	934472				916348	912765		964709		
·		HDTAY23 		HDTAY23	_			HD1B048					HDTBR50	HDTBY88				HDIDC53	HDTEI19		HDTES50		

509	507	162	172	507	507	473	151	166	171	379	178	6	6	6	188	133	106	278	142	92	92	133	133	194	466	89		546
309	361	34	53	304	286	327	50	68	109	308	128	77	68	68	229	183	135	328	165	121	139	165	162	226	386	21		430
61%	%59	62%	%09	41%	35%	40%	20%	21%	47%	37%	52%	43%	40%	37%	27%	47%	%09	47%	75%	%09	43%	54%	%09	54%	2.02	5.7		12.87
				-14			-					gi 2370202 emb CAA	75002.1												PF00052	PF00130		PF00018
thread protein AD7c-NTP	[Homo sapiens]											procollagen alpha 2(V)	[Homo sapiens]												PFAM: Laminin B (Domain IV)	PFAM: Phorbol esters/	diacylglycerol binding domain	PFAM: Src homology
				71. 2								blastx.14													HMMER 1.8	HMMER	1.8	HMMER
				·				**************************************			-	2032			-									,	2036	2037		2044
-												9/255/4													799834	913787		886936
											117.0017244	HD11244							-	· ·				# CIT (11)	HD13137	HDTJJ02		HDTKQ14

	555	291	222	636	399	399	399	411	369	381	636	324	641	995	995	695	695	578	605	695	695	695	569	695	989	989	651	642	491
	439	192	154	49	49	49	70	49	49	70	115	49	372	375	375	375	372	372	372	375	279	372	375	375	547	547	538	547	375
	100%	26%	96.3	48%	65%	%99	%99	%59	62%	64%	47%	28%	42%	20%	47%	47%	48%	43%	42%	46%	35%	43%	43%	46%	63%	63%	52%	26%	35%
	emb CAB41255.1		PF00096	emb CAA38920.1																									
domain 3	(AL049683) hypothetical	protein [Homo sapiens]	PFAM: Zinc finger, C2H2 type	Zfp-29 [Mus musculus]	-	nede Avenue and																							
1.8	blastx.2		HMMER 2.1.1	blastx.2							•																		
	·		2052																								··· ··· · · · · · · · · · · · · · · ·		
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<i>L</i> 99	428	303	228	92	41	148	437	246	173	207	210	21		_	198	2		230	91	233	9	174	241	312		533	629
641	460	338	290	154	82	219	294	136	120	172	10	2			320)		274	129	271	44	206	44	247		213	6
%99	93%	20%	33%	38%	. 20%	29%	%02	40%	030%	83%	52%	, ,			29%			53%	38%	53%	30%	27%	46%	20%		42.5	%96
	gi 1869859 emb CAB	06722.1					gi 1825586 gb AAB4	2222.1	pi 3043919 oh AAC1	3265.1	gi 4426837 gb AAD2	0564.1			gi 179339 gb AAA35	585.1		gi 1247469 emb CAA	01862.1	,			pir/B25313 GNLRL1			PF00169	emb CAB65966.1
	very large tegument	protein [human	herpesvirus 2]				contains similarity to C2	domains Caenorhabditis	(AF034970) docking	protein [Homo sapiens]	(AF108420) 1-	aminocyclopropane-	carboxilate synthase	[Fugu rubripes]	HLA-B-associated	transcript 2 (BAT2)	[Homo sapiens]	TGR-CL5bis [Homo	sapiens]				retrovirus-related reverse	transcriptase pseudogene -	TO THE TALL THE TENT TO THE	PFAM: PH domain	(AJ250425) Collybistin I [Rattus norvegicus]
	blastx.14					,	blastx.14		blastx.14		blastx.14				blastx.14			blastx.14			-		blastx.14		TIN AN ATT	HMMEK 2.1.1	blastx.2
	2091			·			2092	- 14	2113		2118				2121			2131					9562		21.45	7147	
00000	963538	-				,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	920911		959581		839986				006596			919200					961148		020705	50/056	
THOMA 10	HEOMG48					00000	HEOMG/8		HEOMS08		HEOMT79				HEOMU79			HEOMX92				COLEN FOLIATI	HEOMX92		HEONO10	TIEONQ19	

79	379	364		346	334	250	134	237	6	6(-0:	9(22	9;	2	نۃ	5	1	5	84	<u> </u>	4		<u>ن</u>
2,	ώ	3(35	33	2;		2)9	609	480	306	582	1026	152	145	145	267	325	∞	20	264	81	203
163	284	320	142	429	429	273	208	169	139	139	139	154	196	250	30	101	101	232	284	58	180	223	58	180
51%	20%	5.32	38%	32%	31%	75%	36%	6.98	37%	33%	35%	52%	29%	420.7	51%	53%	46%	20%	20%	55%	55%	42%	62%	62%
dbj BAA91707.1		PF00099	gi 214044 gb AAA49	679.1	•			PF00096	dbj BAA91884.1					PF00144	gi 475909 emb CAA4 7472.1	gi 1732471 gb AAB4	9656.1						-	
(AK001463) unnamed	protein product [Homo sapiens]	PFAM: Zinc-binding metalloprotease domain	alpha-1 type II collagen	[Xenopus laevis]				PFAM: Zinc finger, C2H2 type	(AK001753) unnamed	protein product [Homo	sapiens]			PFAM: Beta-lactamase	ORF1A [Homo sapiens]	rehydrin [Tortula ruralis]	e e e e e e e e e e e e e e e e e e e							
blastx.2		HMMER 1.8	blastx.14					HMMER 2.1.1	blastx.2			 		HMMER 2.1.1	blastx.14	blastx.14		_						
2148		2157	2174					2189						2203	2204	2214								
949152		851009	958184			_		909032						942596	965930	959572								
HEONV59		HEOPE58	HEOPO08					HE0QC76						HEOQP44	HEOQS11	HEORE79								

174	1801	156	417	114	114 297	06	708	288	421	448	186	144
302	1202	115	226	25	235	64	526	88	233	212	103	13
65%	99%	4.1	95%	12.86	52%	3.27	30.41	11.81	166.4	%68	10.48	29%
gi 3170182 gb AAC1	gi 5881961 gb AAD5	PF00130	gi 5823554 gb AAD5 3184 1 AF180920 1	PF00035	gi 158506 gb AAA73 062.1	PF00130	PF00018	PF00183	PF01352	gi 506502 emb CAA5 6225.11	PF00435	gi 5689158 dbj BAA8
(AF039691) antigen NY-	(AF064257) Dhm1-like	PFAM: Phorbol esters / diacylglycerol binding	(AF180920) cyclin ania- 6a [Homo sapiens]	PFAM: Double-stranded RNA binding motif	[D.melanogaster mRNA, complete cds.], gene product [Drosophila melanogaster]	PFAM: Phorbol esters / diacylglycerol binding domain	PFAM: Src homology domain 3	PFAM: Heat shock hsp90 proteins	PFAM: KRAB box	NK10 [Mus musculus]	PFAM: Spectrin alpha chain, repeated domain	(AB023622) Septin6 [Mus
blastx.14	blastx.14	HMMER 1.8	blastx.14	HMMER 1.8	blastx.14	HMMER 1.8	HMMER 1.8	HMMER 1.8	HMMER 2.1.1	blastx.14	HMMER 1.8	blastx.14
2250	2267	2279	2282	2302		2346	2354	2381	2392		2400	
915285	952455	923895	961974	919630		871911	932851	783820	<i>1</i> 95806		602596	
HHECO01	HHEEC07	ннени73	ННЕЈНЗ0	HHEND45		ннеоко1	ннедуз9	HHESU85	HHETQ54		HHEUA62	***

92	37	782	123		123	372		340	104		284	, l	330	6	162	176	203	124	317	115	72	317	352
3	111	129	82			277		107	3	· · · · · · · · · · · · · · · · · · ·	264	·	440	47	115	165	174	68	355	68	107	349	387
										·····													<u>~</u>
31.5	2.17	92%	1.99		48.1	78%		82%	100%		2.86		%68	%69	43%	100%	70%	20%	61%	44%	28%	63%	20%
								3					2										
		gi 5059425 gb AAD3 9005.1 AF156884_1				gi 5020264 gb AAD3	1363_1	gi 1651236 dbj BAA3					gi 2766165 dbj BAA2		gi 334072 gb AAA47			gi 159657 gb AAA29					
0023	6600	gi 5059425 gb AAD;	130		449	20264 g	8043.1 AF151363_1	51236 d		-	660		66165 d	<u>-1</u> :	4072 gb	! —-		9657 gb					
PF00023	PF00099	gi 50 9005	PF00130	····	PF01449	gi 50	8043	gi 16	5202.1		PF00099		gi 27	4267.1	gi 33	471.1		gi 15	371.1				
 	ing	ike iens]	sters /	ding		2	protein		eceptor	ırsor.	ng	main	ام			s]		[unns					
nk repea	nc-bind stease do	4) RIP-1	orbol es	erol bin	osphate otein	3) Cdc4	stivating sulus]	sal	age n4 r	rA precuia colil	nc-bindi	tease do	O) CDE	iens]	tein	ies viru		Ascaris s					
PFAM: Ank repeat	PFAM: Zinc-binding metalloprotease domain	(AF156884) RIP-like kinase [Homo sapiens]	PFAM: Phorbol esters	diacylglycerol binding domain	PFAM: Phosphate-binding protein	(AF151363) Cdc42	GTPase-activating protein [Mus musculus]	Hypothetical	bacteriophage n4 receptor	protein NfrA precursor. [Escherichia coli]	PFAM: Zinc-binding	metalloprotease domain	(AB008430) CDEF	Homo sapiens	ORF-3 protein	[Pseudorabies virus]		collagen [Ascaris suum]					
		ļ · · ·					<u> </u>	F	<u>قہ</u> —	<u>a</u> :	-	u u	_										_
HMMER 2.1.1	HMMER 1.8	blastx.14	HMMER	1.8	HMMER 2.1.1	blastx.14		blastx.14			HMMER	1.8	blastx.14		blastx.14			blastx.14					ļ
2401	2486	2526	2529		2572	2600		2633			2641		2679		2694			2697					
795268	963724	950728	531053		531228	999606		967636			531054		950096		920292			932127			-		
79.	.96	95(53]		53]	506		/96			531		96		920			932		T-1			_
HHEUC31	HKBAT27	HLMBW11	HLMBY16		HLMDU71	HLMFU09		HLMHP67			HLMHT94		HLMIX95		HLMMA52			HLMMD05					
HHE	HKE	HLN	HLN		HLN	HLN		HLM			HLM		HLM		HLM			HLM					

317	366	317	99	115	317	322	382	384	448	419	256	146	138	231	289	153	57	208	260	15	158	293	191	215	156	182	<u>ر</u>
358	407	355	110	189	355	245	230	337	404	378	173	66	19	184	345	191	98	306	162	68	229	376	259	283	179	232	26
42%	20%	46%	46%	32%	46%	17.86	62%	81%	%98	71%	39%	43%	%02	37%	36%	53%	20%	33%	37.3	44%	37%	35%	30%	39%	75%	47%	15%
						PF00023	gi 488505 dbj BAA06	418.1			-		gi 687206 gb AAA63	589.1	gi 4494984 gb AAD2	1406.1	-		PF00169	gi 334072 gb AAA47	471.1			44-14-14		- 1	•
						PFAM: Ank repeat	similar to HUMORFU	(D26069) [Homo sapiens]					dynein heavy chain	isotype 6 [Tripneustes gratilla]	(AF083501) latent nuclear	antigen [Macaca mulatta	rhadinovirus 17577]		PFAM: PH domain	ORF-3 protein	[Pseudorabies virus]						
						HMMER 1.8	blastx.14						blastx.14		blastx.14				HMMER 2.1.1	blastx.14							
						2733							2769	. 117	2776				2871	2980	_						
						926188							964739		92026				909874	998606							
						HLMMV66	· · · · · · · · · · · · · · · · · · ·						HLMNL55		HLMNN02				HLYAA41	HLYDL60							

197	161	3	124	406	292 504	400)	74		234	314	300	385	_	231		403	228	271	407	
250	223	200	68	188	113	383)	12		-	264		347		157		281	154	233	210	
38%	38%	39%	4.11	58.6	41%	2 86)	24.4		%59	47%	100%	%92		24.8		36%	26%	61%	128.8	
		gi 473842 gb AAA20 666.1	PF00096	PF00169	gb AAC35236.1	PF00130		PF00612		sp BAA33720 BAA3	3720	gi 1651427 dbj BAA3	5638.1		PF00025		gi 3746799 gb AAC6	4063.1		PF00204	
		orfIV [Borna disease virus]	PFAM: Zinc finger, C2H2 type	PFAM: PH domain	(AC005496) unknown protein [Arabidopsis	PFAM: Phorbol esters /	diacylglycerol binding domain	PFAM: IQ calmodulin-	binding motif	EDTP(egg derived	tyrosine phosphatase).	Formate c-	acetyltransferase (EC	coli]	PFAM: ADP-ribosylation	ractor family	(AF082517) ADP-	ribosylation factor	[Entamoeba histolytica]	PFAM: DNA	topoisomerase II (N-terminal region)
		blastx.14	HMMER 1.8	HMMER 2.1.1	blastx.2	HMMER	1.8	HMMER	2.1.1	blastx.14		blastx.14			HMMER	2.1.1	blastx.14			HMMER	2.1.1
		2986	2991	2993		3005		3042		3056		3062			3063					3065	
		966732	526245	927872		682176		832311		920551		968199			907640					729831	
		HLYDS11	HLYDT68	HLYDV62		HLYEN93		HLYGP46		HLYHN67		HMAAF10			HMABJ56					HMABQ71	

	920088	3067	blastx.14	ORF_f418 [Escherichia	gi 536985 gb AAA97	%56	202	143
\top				coli	040.1			
	939916	3071	blastx.2	(AK002022) unnamed	dbj BAA92041.1	%86	270	728
				protein product [Homo sapiens]				
	778521	3078	HMMER 2.1.1	PFAM: WH1 domain	PF00568	06	46	303
	723186	3080	HMMER 1.8	PFAM: Signal C termial domain	PF00512	40.87	31	405
	947905	3085	HMMER 2.1.1	PFAM: Peptidase family M3	PF01432	62.9	115	402
			blastx.14	CG Site No. 18031	gi 466635 gb AAB18	84%	112	390
		· · · · · · · · · · · · · · · · · · ·		[Escherichia coli]	474.1	100%	2	112
T	000330	0220	1-10-4-11	M. T. T. T. T. T.		35%	363	422
	707006	6066	ofastx.14	Maob [Escherichia coli]	gi[1480003 db] BAA1	%66 %66	1516	803
				-	1058.1	%06	1673	1545
	956195	3091	HMMER	PFAM: Adenylate kinases	PF00406	50.17	63	296
+	895981	3107	blastx.2	(A.1007798) stromal	emb[CAB50367 1]	7008	90	751
				antigen 3, (STAG3)		%06 %75	445	573
				[Homo sapiens]		71%	10	168
	963794	3110	blastx.14	probable transposase -	pir S72481 S72481	73%	183	320
_				human transposon MER37		82%	119	187
						43%	313	423
						61%	2	58
7						63%	06	122
	753133	3117	HMMER 2.1.1	PFAM: Kelch motif	PF01344	51.9	7	132
\dashv	462502	3127	HMMER	PFAM: Zinc-binding	PF00099	3.49	166	183

HMMAC19 953580 3129 blastx.14 (AF003535) ORF2-like gi[2197085]gb]AAD0 HMMCH04 944069 3208 blastx.2 unknown [Homo sapiens] gb]AAC50940.1 HMQBU96 765162 3247 HMMER FRAM; Helix-loop-helix PF00010 HMQBU96 765162 3247 HMMER PFAM; Helix-loop-helix PF00010 HMQDZ19 940694 3267 blastx.14 urokinase plasminogen gi[43390]emb[CAA5 HMQBV28 970579 3303 blastx.14 YKL249 [Saccharomyces gi[871536]emb[CAA4 HMSBV28 970579 3303 blastx.14 YKL249 [Saccharomyces gi[871536]emb[CAA4 HMSBV28 970579 3303 blastx.2 (AC00018 PF00018 HMSCD15 918133 3310 HMMER PFAM; Src homology PF00125 HMSFR69 738588 3373 HMMER PFAM; Bacterial mutT PF00293 HMSGL27 855759 9573 HMMER PFAM; Bacterial mutT PF00293 HMSGP73				1.8	metalloprotease domain				
4 944069 3208 blastx.2 unknown [Homo sapiens]	MAC19	953580	3129	blastx.14	(AF003535) ORF2-like	gil2197085lgblAAD0	47%	96	145
4 944069 3208 blastx.2 unknown [Homo sapiens] 765162 3247 HMMER PFAM: Helix-loop-helix 940694 3267 blastx.14 urokinase plasminogen 970579 3303 blastx.14 YKL249 [Saccharomyces cerevisiae] Cerevisiae] 1.8 domain 3 blastx.2 (AK000975) unnamed protein product [Homo sapiens] 738588 3373 HMMER PFAM: Src homology 1.8 H2A, H2B, H3 and H4 855759 9573 HMMER PFAM: Bacterial mutT 1.8 protein 925385 3401 blastx.14 (AC004490) R29381_1 871492 3413 HMMER PFAM: Ribosomal protein 1.8 protein 1.8 4 746582 3431 HMMER PFAM: Ribosomal protein 1.8 domain 3 domain 3			_		protein [Homo sapiens]	4635.1	47%	282	344
4 944069 3208 blastx.2 unknown [Homo sapiens] 765162 3247 HMMER PFAM: Helix-loop-helix 1.8 DNA-binding domain 940694 3267 blastx.14 urokinase plasminogen activator receptor [Homo sapiens] cerevisiae] 970579 3303 blastx.14 YKL249 [Saccharomyces cerevisiae] cerevisiae] l.8 blastx.2 (AK000975) unnamed protein product [Homo sapiens] 1.8 HZA, HZB, H3 and H4 855759 9573 HMMER PFAM: Bacterial mutT 1.8 HZA, HZB, H3 and H4 855759 9573 HMMER PFAM: Bacterial mutT 1.8 protein protein 925385 3401 blastx.14 (AC004490) R29381_1 871492 3413 HMMER PFAM: Ribosomal protein 1.8 protein 1.8 4 746582 3431 HMMER PFAM: Src homology 1.8 domain 3 domain 3 blastx							87%	187	210
765162 3247 HMMER PFAM: Helix-loop-helix 940694 3267 blastx.14 urokinase plasminogen 970579 3303 blastx.14 YKL249 [Saccharomyces cerevisiae] 970579 3303 blastx.14 YKL249 [Saccharomyces cerevisiae] 1.8 domain 3 1.8 domain 3 1.8 domain 3 1.8 HMMER PFAM: Src homology 1.8 HOMOOT5 unnamed 1.8 HOMOOT5 unnamed 1.8 HOMOOT5 unnamed 1.8 HOMOOT5 unnamed 1.8 HOMOOT5 unnamed 1.8 HAM. Core histones 1.8 HAM. Bacterial mut 1.8 PFAM: Ribosomal protein 1.8 S12 1.8 S12 1.8 S12 1.8 S12 1.8 S12 1.8 S12 1.8 S12 1.8 Gomain 3 1.8 Gomain 4 208	blastx.2	unknown [Homo sapiens]	gb AAC50940.1	28%	423	089			
940694 3267 blastx.14 urokinase plasminogen sapiens] 970579 3303 blastx.14 YKL249 [Saccharomyces cerevisiae] 5 918133 3310 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AK000975) unnamed protein product [Homo sapiens] 738588 3373 HMMER PFAM: Core histones 1.8 HZA, HZB, H3 and H4 855759 9573 HMMER PFAM: Bacterial mutT 1.8 protein 925385 3401 blastx.14 (AC004490) R29381_1 [Homo sapiens] 871492 3413 HMMER PFAM: Ribosomal protein 1.8 S12 4 746582 3431 HMMER PFAM: Src homology 1.8 S12 blastx.2 (AF030131) Plenty of guran, and and and and and and and and and and	1QBU96	765162	3247	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	7.33	8	40
activator receptor [Homo sapiens] 970579 3303 blastx.14 YKL249 [Saccharomyces cerevisiae] 5 918133 3310 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AK000975) unnamed protein product [Homo sapiens] 1.8 HMMER PFAM: Core histones 1.8 HZA, H2B, H3 and H4 855759 9573 HMMER PFAM: Bacterial mutT 1.8 protein 925385 3401 blastx.14 (AC004490) R29381_1 Homo sapiens] 871492 3413 HMMER PFAM: Ribosomal protein 1.8 S12 HMMER PFAM: Src homology 1.8 S12 HMMER PFAM: Src homology 1.8 S12 HMMER PFAM: Src homology 1.8 S12 A6030131) Plenty of EU25. DOG! LMA.	4QDZ19	940694	3267	blastx.14	urokinase plasminogen	gi 433901 emb CAA5	100%	68	124
970579 3303 blastx.14 YKL249 [Saccharomyces cerevisiae] 5 918133 3310 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AK000975) unnamed protein product [Homo sapiens] 738588 3373 HMMER PFAM: Core histones 1.8 HZA, HZB, H3 and H4 855759 9573 HMMER PFAM: Bacterial mutT 1.8 protein 925385 3401 blastx.14 (AC004490) R29381_1 [Homo sapiens] 871492 3413 HMMER PFAM: Ribosomal protein 1.8 S12 4 746582 3431 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AF030131) Plenty of grant and an and an and an and an and an and an and an and an and an and an and an and an and an an and an an an an an an an an an an an an an					activator receptor [Homo sapiens]	2191.1	91%	133	168
Secretisiae Cerevisiae Ce	ASBV28	970579	3303	blastx.14	YKL249 [Saccharomyces	gi 871536 emb CAA4	92%	260	108
5 918133 3310 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AK000975) unnamed protein product [Homo sapiens] 738588 3373 HMMER PFAM: Core histones 1.8 H2A, H2B, H3 and H4 855759 9573 HMMER PFAM: Bacterial mutT 1.8 protein 925385 3401 blastx.14 (AC004490) R29381_1 [Homo sapiens] 871492 3413 HMMER PFAM: Ribosomal protein 1.8 S12 4 746582 3431 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AF030131) Plenty of					cerevisiae]	9304.1	51%	141	1
blastx.2 (AK000975) unnamed protein product [Homo sapiens] 738588 3373 HMMER PFAM: Core histones 1.8 H2A, H2B, H3 and H4 855759 9573 HMMER PFAM: Bacterial mutT 1.8 protein 871492 3413 HMMER PFAM: Ribosomal protein 1.8 S12 4 746582 3431 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AF030131) Plenty of	IMSCD15	918133	3310	HMMER 1.8	PFAM: Src homology domain 3	PF00018	41.06	453	599
protein product [Homo sapiens] protein product [Homo sapiens] 738588 3373 HMMER PFAM: Core histones 855759 9573 HMMER PFAM: Bacterial mutT 925385 3401 blastx.14 (AC004490) R29381_1 871492 3413 HMMER PFAM: Ribosomal protein 4 746582 3431 HMMER PFAM: Src homology 1.8 31.8 S12 4 746582 3431 HMMER PFAM: Src homology blastx.2 (AF030131) Plenty of CH70. DOCH DATE DATE DATE DATE DATE DATE DATE DATE				blastx.2	(AK000975) unnamed	dbj BAA91451.1	%86	453	635
738588 3373 HMMER PFAM: Core histones 855759 9573 HMMER PFAM: Bacterial mutT 925385 3401 blastx.14 (AC004490) R29381_1 871492 3413 HMMER PFAM: Ribosomal protein 4 746582 3431 HMMER PFAM: Src homology blastx.2 (AF030131) Plenty of CH32., BOSULERALE					protein product [Homo		29%	387	479
738588 3373 HMMER PFAM: Core histones 855759 9573 HMMER PFAM: Bacterial mutT 925385 3401 blastx.14 (AC004490) R29381_1 871492 3413 HMMER PFAM: Ribosomal protein 4 746582 3431 HMMER PFAM: Src homology blastx.2 (AF030131) Plenty of CH70. DOCH DATE					sapiens]		78%	80	175
855759 9573 HMMER PFAM: Bacterial mutT 925385 3401 blastx.14 (AC004490) R29381_1 871492 3413 HMMER PFAM: Ribosomal protein 4 746582 3431 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AF030131) Plenty of CH32., POSUL PAL:	ASFR69	738588	3373	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	7.78	258	202
925385 3401 blastx.14 (AC004490) R29381_1 871492 3413 HMMER PFAM: Ribosomal protein 1.8 S12 4 746582 3431 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AF030131) Plenty of	ASGL27	855759	9573	HMMER 1.8	PFAM: Bacterial mutT	PF00293	5.56	276	202
871492 3413 HMMER PFAM: Ribosomal protein 4 746582 3431 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AF030131) Plenty of	4SGP73	925385	3401	blastx.14	(AC004490) R29381_1 [Homo sapiens]	gi 2995577 gb AAC0 8316.1	94%	141	908
746582 3431 HMMER PFAM: Src homology 1.8 domain 3 blastx.2 (AF030131) Plenty of	4SGX14	871492	3413	HMMER 1.8	PFAM: Ribosomal protein S12	PF00164	33.44	28	153
(AF030131) Plenty of SU22: POSUI PAGE	MSHO64	746582	3431	HMMER 1.8	PFAM: Src homology domain 3	PF00018	11.08	316	405
SUDS, FOST INIUS				blastx.2	(AF030131) Plenty of SH3s; POSH [Mus	gb AAC40070.1	47%		411

				musculus				
	733386	3447	HMMER 1.8	PFAM: Zinc finger, CCHC class	PF00098	4.89	208	228
	200596	3491	blastx.14	(AF148805) latent nuclear antigen [Kaposis sarcoma-	gi 5669894 gb AAD4 6501 1 AF148805 6	20%	667	1137
				associated herpesvirus]		21%	241	465
						23%	211	453
[0007					16%	139	465
7	744990	3498	HMMER 2.1.1	PFAM: BAH domain	PF01426	48.7	7	163
6	959413	3509	blastx.14	(AF094516) E1-like protein [Homo sapiens]	gi 3820614 gb AAC6 9630.1	%26	76	513
9	958216	3538	blastx.14	(AF082556) TRF1-	gi 3929219 gb AAC7	%9L	2	232
				interacting ankyrin-related ADP-ribose polymerase [Homo sapiens]	9841.1			-
اري	948130	9578	blastx.2	(AF118082) PRO1902	gb AAF22026.1 AF1	64%	302	463
				[Homo sapiens]	18094_21	63%	462	527
						%88	532	558
6	948202	3548	blastx.14	cDNA EST	gi 3879085 emb CAA	48%	514	612
				EMBL:M89462 comes	94301.1	39%	365	463
				from this gene; cDNA		36%	799	355
				EST 1 1 yk349d7.5 comes		39%	173	256
				from this gene; cDNA		26%	514	591
				EST yk358b9.5 comes from this				
6	904807	3589	HMMER	PFAM: Core histones	PF00125	13.38	1252	1329
۱۶	7,077	2000	1.0	112A, 112B, 113 allu 114				
2	924634	9095	blastx.14	Emf1 alpha [Ephydatia	gi 9300 emb CAA494	%05	19	84
				muelleri]	72.1	33%	66	233
- 1						%99	217	243

~	3610	blastx.14	(AF175223) SANT	oi 5815245 oh AAD5	/003		
~	3612	·	domain protein SMRTER [Drosophila melanogaster]	2614.1 AF175223_1	53%	122	84
		HMMER 1.8	PFAM: Low-density lipoprotein receptor domain class A	PF00057	41.61	171	245
		blastx.14	(AF110520) NG29 [Mus	gi 4050096 gb AAC9	%69%	114	239
			musculus]	/969.1	35%	129 6	239
					20%	72	107
HMWGG55 920575	3642	blastx.14	DNA polymerase [Pyrococcus furiosus]	gi 216918 dbj BAA02 362.1	94%	195	308
HMWGT07 953454	3645	blastx.14	(AL078579) putative	gi 4972120 emb CAB	40%	218	322
-			protein [Arabidopsis	43977.1	40%	395	475
			thaliana		46%	113	157
HMWHN70 851334	3654	HMMER	PFAM: Zinc finger,	PF00097	6.51	187	255
		1.8	C3HC4 type (RING finger)				
HNEBJ08 958742	3689	blastx.14	mucin 2 precursor,	pir A49963 A43932	35%	305	264
		:	intestinal - human (fragments)		83%	320	303
HNEDU01 909832	3748	blastx.14	(AC002398) F25965_3	gi 2477513 gb AAB8	71%	207	323
			[Homo sapiens]	1198.1	21%	80	205
					62%		87
					43%	323	412
					20%	337	384
HNFEF95 971171	3792	blastx.14	ORF_0493 [Escherichia	gi 606260 gb AAA58	%86	548	201
			coli]	123.1	%68	103	20
+					81%	185	105
HNFFM25 705856	3818	HMMER	PFAM: Laminin B	PF00052	0.47	520	603

			1.8	(Domain IV)				
HNFFT62	574623	3828	HMMER 1.8	PFAM: C2 domain	PF00168	2.74	207	272
HNFGI01	921431	3851	blastx.14	(AF118890) s-tomosyn	gi 4689231 gb AAD2	%98	234	302
				isoform [Rattus norvegicus]	7819.1 AF118890_1	100%	153 287	200
HNFGI49	202606	3852	blastx.14	(AF086624) serine	gi 3800869 gb AAC6	100%		45
				threonine kinase [Rattus	8900.1	100%	09	98
HNFGM76	599806	3862	HMMER	PFAM: Zinc finger, C2H2	PF00096	74.8	232	306
			2.1.1	type)
			blastx.2	(AF132599) RANTES	gb AAD26864.1 AF1	95%	-	417
		······		factor of late activated T	32599_1			
			······································	lymphocytes-1 [Homo sapiens]				
HNFHA11	967520	3874	HMMER	PFAM:	PF01293	118.1	55	219
			2.1.1	Phosphoenolpyruvate				
				carboxykinase				
			blastx.14	phosphoenolpyruvate	gi 606337 gb AAA58	%66	55	360
				carboxykinase [Escherichia coli]	200.1			
HNFHK77	576186	3890	HMMER	PFAM: Aldehyde	PF00171	30.2	231	326
			2.1.1	dehydrogenase family			-	
HINFHQ01	938114	3897	blastx.14	serine/threonine kinase	gi 758593 emb CAA8	28%	248	331
			,	with SH3 domain, leucine	8531.1	46%	43	81
				1		46%	371	415
<i>-</i>						25%	79	186
						41%	176	211
HNFHW14	939763	3908	HMMER 2.1.1	PFAM: Latrophilin/CL-1-like GPS domain	PF01825	35.1	44	196

			blastx.2	(AF166382) serpentine	gb AAF00617.1 AF1	44%	38	283
				receptor [Mus musculus]	66382_1			
HNFIG07	918389	3921	blastx.14	(AF128881) PI3 kinase	gi 4928058 gb AAD3	%08	2	445
				regulatory subunit P101	3397.1 AF128881_1	%09	448	477
o) arar ar	000000	, , ,	,	Tround sapiens				
HINFIP50	965283	3936	blastx.14	mutant sterol regulatory	gi 841318 gb AAA85	92%	356	631
	1.1			element binding protein-2	718.1	34%	42	128
				1		85%	999	685
HNGAL92	623886	3976	blastx.14	phosphatidylserine	gi 551827 gb AAA83	73%	212	18
				decarboxylase	896.1			
				[Escherichia coli]				
HNGAS51	773208	3984	HMMER	PFAM: Zinc-binding	PF00099	2.57	144	182
			1.8	metalloprotease domain				
HNGBF80	574475	4001	HMMER	PFAM: Zinc finger, C2H2	PF00096	4.98	88	111
			1.8	type				
HNGBH77	577361	4005	HMMER	PFAM: ATP synthase A	PF00119	9.81	130	189
			1.8	chain				
HNGCE85	970738	4039	blastx.14	hypothetical protein	pir S72489 S72489	72%	284	210
	,			Tigger 2 - human		63%	212	180
				transposon MER37 1				
HNGCX07	953900	4065	HMMER	PFAM: Src homology	PF00018	3.68	45	161
			1.8	domain 3				
HNGEN37	663955	4160	HMMER	PFAM: Indole-3-glycerol	PF00218	125.4	2	223
			2.1.1	phosphate synthases				
HNGEQ07	953647	4169	HMMER	PFAM: TPR Domain	PF00515	10.86	164	238
INICED 42	500201	4177	TTATATE	DEANG DEALEST AT	200000		,	
HINGER45	099391	41/3	HMMEK 1.8	FFAM: Bacterial mut1 protein	PF00293	3.79	151	195
HNGER96	95236	4177	blastx.14	Bkm-like protein	gi 552132 gb AAA28	%09	250	294
				Drosophila melanogaster]	872.1	64%	250	291

HMMER PFAM: Helicases 1.8 conserved C-terminal domain
blastx.14 adenine phosphoribosyltransferase [Escherichia coli]
HMMER PFAM: Zinc finger, C2H2 1.8 type
HMMER PFAM: Bacterial 1.8 regulatory proteins, luxR family
blastx.14 collagen [Ascaris suum]
HMMER PFAM: ABC transporters 1.8
blastx.2 MsbA protein. [Escherichia coli]
HMMER PFAM: ABC transporters 1.8
blastx.2 MsbA protein. [Escherichia coli]
HMMER PFAM: ABC transporters 1.8
blastx.2 MsbA protein.

162	242	512	10	87	161	198	215	290	422	75	•	155	129	129		129	306	132	132	167	164	248	63	129	129
25	1 60		84	116	205	263	84	102	96		ı	196	167	155	75	152	335	152	152	196	196	289	131	152	152
84%	6.09	%66	44%	%09	40%	36%	42.7	55.68	44%	%09		20%	53%	%99	36%	75%	%09	85%	85%	%09	54%	20%	79%	62%	75%
	PF00664	dbj BAA35658.1	pir S28303 S28303				PF00665	PF00075	gi 930259 emb CAA3	3367.1		gi 1877435 gb AAB5	1499.1					•							
[Escherichia coli]	PFAM: ABC transporter transmembrane region.	MsbA protein. [Escherichia coli]	hypothetical protein	T23G5.2 - Caenorhabditis	elegans		PFAM: Integrase core domain	PFAM: RNase H	reverse transcriptase (476	AA) [Woolly monkey	sarcoma virus]	180 kDa bullous	pemphigoid antigen 2/type	XVII collagen [Homo	sapiens]										
	HMMER 2.1.1	blastx.2	blastx.14				HMMER 2.1.1	HMMER 1.8	blastx.14			blastx.14		_			<u> </u>								
	9896		4244	·			4246	4265				4270													
	943115		935135	·			526792	971170				924693													
	HNGFK28		HNGF046			200001	HNGFO81	HNGFU12				HNGFW09													

129	129	129	164	397	115	341	347	206	206	59	103	206	441	58	177	293	342	114	286	40	105	286	225	13	1	332	318
152	155	155	193	356	47	285	288	171	171	9	53	171	424	14	254	168	280	73	336	93	155	327	799	87	81	355	286
75%	%99	%99	%09	20%	34%	. 45%	40%	20%	28%	38%	41%	20%	0.51	6.36	20%	20%	21%	57%	28%	25%	47%	64%	21%	32%	33%	62%	6.75
				gi 388625 gb AAA36	968.1								PF00052	PF00096	gi 1196398 gb AAA8 8020.1	gi 56588 emb CAA37	645.1		gi 495866 gb AAA58	965.1			,				PF00049
				type VII collagen	[Cricetulus griseus]								PFAM: Laminin B (Domain IV)	PFAM: Zinc finger, C2H2 type	unknown protein [Homo sapiens]	ORF2 [Rattus norvegicus]			collagen type VII [Homo	sapiens]							PFAM:
				blastx.14									HMMER 1.8	HMMER 1.8	blastx.14	blastx.14			blastx.14								HMMER
				4306			_						4317	4340	4450	4483			4630								4662
				924908									964819	765698	935706	916748			952221								835972
				HNGCH78									HNGGM10	HNGGR74	HNGHT06	HNGIJ01			HNGKE07								HNGLE52

																		_							
	599	599	249	47	136	362		3	116		161	323	272	145	•		347		427		170	169	164	15	53
	348	270	416	193	258	237		104	151		262	406	310	113			228		395		33	23	9	47	91
	47.92	%86	%86	71%	63%	8.41		94%	91%		38%	28%	53%	4.4		_	8.4		1.89		50%	44%	41%	54%	46%
	PF00005	dbj BAA35501.1	gi 455170 gb AAA83	861.1		PF00119		gi 1790156 gb AAC7	6742.1		gi 4469304 emb CAA	25493.1		PF00271			PF00119	DE00120	FF00130	****	gi 1196398 gb AAA8	8020.1		pir A27695 A27695	-
Insulin/IGF/Relaxin family	PFAM: ABC transporters	Hypothetical protein HI0658 [Escherichia coli1	diaminopimelate	decarboxylase	[Escherichia coli]	PFAM: ATP synthase A	chain	(AE000449) putative	xylanase Escherichia	1 111	plot carboxyterminal	sequence [Kirsten murine	sarcoma virus]	PFAM: Helicases	conserved C-terminal	domain	PFAM: ATP synthase A	DEAM: Dhoubel estant	dioxilational hinding	dacyigiyesioi oinding domain	unknown protein [Homo	sapiens]		synexin - bovine	(fragment)
1.8	HMMER 1.8	blastx.2	blastx.14			HMMER	1.8	blastx.14		1.1 1.4	blastx.14			HMMER	1.8		HMMER	HMMEB	1.8	0.1	blastx.14			blastx.14	
	4666	·	4668	***		4715		4762		1700	4/90			4798			4823	4878	2		4910			4955	
	839088		954140			806036		953888		077270	90/06			724404			774280	506621	1		924211			964882	
	HNGLG06		HNGLH82		10000	HNGMM87	20000141	HNG0022		HNH A 111				HNHBEI9			HNHBY45	HNHDM74			HNHDY50			HNHEJ85	

43% 250 203	207 212 342	207 212 342 342 164 227 295	207 212 342 342 227 295 259 346 268 268 259 367 367	207 212 342 342 227 295 259 346 268 268 259 367 367 367 367	207 212 342 342 227 227 227 228 259 367 367 367 367 367 367 367 367 367 367	207 212 342 342 346 227 295 259 367 367 367 367 367 367 367 367 367 367

06591.1	gl 486843/ gb AAD3 1316.1 AF144054_1	gi 486843 / gb AAD3 1316.1 AF144054_1 gi 2981221 gb AAC0 6254.1	486843 gp AAD3 316.1 AF144054_1 2981221 gb AAC0 254.1	gl 486843 [gb AAD3 1316.1 AF144054_1 gi 2981221 gb AAC0 6254.1 sp Q9Y6Y5 Q9Y6Y5	gl 480843 gp AAD3 gp A8054_1 gi 2981221 gb AAC0 6254.1 sp Q9Y6Y5 Q9Y6Y5 gi 1841543 gb AAC6 3097.1	4868437 gp AALD3 16.1 AF144054_1 2981221 gb AAC0 254.1 29876Y5 Q9Y6Y5 1841543 gb AAC6 97.1
+	g1 480845 1316.1 AF			07	37 0000	07 W(1)
protein [Mus musculus]	(AF144054) apoptosis related protein APR-4	(AF144054) apoptosis related protein APR-4 [Homo sapiens] (AF053091) eyelid [Drosophila melanogaster]	AF144054) apoptosis related protein APR-4 Homo sapiens] AF053091) eyelid Drosophila melanogaster	(AF144054) apoptosis related protein APR-4 [Homo sapiens] (AF053091) eyelid [Drosophila melanogaster]	(AF144054) apoptosis related protein APR-4 [Homo sapiens] (AF053091) eyelid [Drosophila melanogaster] IDN4-GGTR14 PROTEIN. notch4 [Homo sapiens]	(AF144054) apoptosis related protein APR-4 [Homo sapiens] (AF053091) eyelid [Drosophila melanogaster] IDN4-GGTR14 PROTEIN. notch4 [Homo sapiens] PFAM: Helicases conserved C-terminal domain
protein blastx.14 (AF14	111	blastx.14 (AF05			4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
5030 blas		5121 blas				
967126	1	953416 5				
HNHFA11	1	HNHGD07				

	7 155	3 148	300		73			235	122		380		70		394			79
220	187	83	49	363	14	262	310	200	06		360		2		77	408	593 83	47
33%	63%	3.57	67.6	%09	45%	50%	47%	2.66	11.1		4.12	•	22.31		100%	50%	50%	54%
		PF00293	PF00607	gi 4680231 gb AAD2	/384.1 AF118275_1	7,76		PF00130	PF00442		PF00076		PF00130		gi 5106956 gb AAD3	9906.1 AF113615_1	gi[339771 gb AAA51	622.1
	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	PFAM: Bacterial mutT protein	PFAM: gag gene protein p24 (core nucleocapsid protein)	(AF118275) atrophin-	Homo sapiens	r .		PFAM: Phorbol esters / diacylglycerol binding	PFAM: Ubiquitin	carboxyl-terminal hydrolases family 2	PFAM: RNA recognition	motif. (aka RRM, RBD, or RNP domain)	PFAM: Phorbol esters /	diacylglycerol binding domain	(AF113615) FH1/FH2	domain-containing protein	ORF2 contains a reverse	transcriptase domain.;
	477 6 411	HMMER 1.8	HMMER 2.1.1	blastx.14				HMMER 1.8	HMMER	1.8	HMMER	1.8	HMMER	1.8	blastx.14		blastx.14	
	7703	9970	5318	5496				5497	5512		5646		5682		9895		5702	
	265500	/02298	908419	934456				935322	866951		471037		660053		68/0/6		954360	
	HNILILII 74	TINTITIE /4	HNHIA95	HNHPH29			11011	HOIAE91	HSATQ28		HSAYN79		HSYBL15		HSYDP04		HT3SA07	

			1.8	homology) domain				
			blocky 14	(AE052074) CIII A D 70				
			Ulasta. 14	(Arussy/4) SWAF-/U	g1 3290154 gb AAC4	53%	251	448
				[Mus musculus]	0155.1	%88	4	54
						33%	448	492
HT5EA69	952359	5721	blastx.14	(AL032624) cDNA EST	gi 3881086 emb CAA	37%	264	470
				yk321h8.5 comes from	21522.1	30%	123	751
-				this gene; 1 from this gene	_))		7
				[Caenorhabditis elegans]				
HTAAW46	719422	5735	HMMER	PFAM: HMG (high	PF00505	5.82	9	35
			1.8	mobility group) box))
HTABG87	940153	5745	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	13.81	240	335
·		_	blastx.14	(AF006064) protein	gi[2393890[gb AAC5	54%	~	139
	···-			kinase homolog [Fowlpox	8236.1	33%	189	356
				virus]				1
HTACW17	961560	2260	blastx.14	(AC007660) unknown	gi 4895220 gb AAD3	37%	54	221
				protein [Arabidopsis	2806.1 AC007660_7	61%	212	265
7722 1 222				thaliana]				
HIAFE69	944409	5797	blastx.2	(AK000496) unnamed	dbj BAA91205.1	%69	432	704
				protein product [Homo				
HTAHL45	908949	5817	HMMER 2.1.1	PFAM: SCAN domain	PF02023	228.7	268	555
			blastx.14	(AC004522) Zn-finger-	gi 3006231 gb AAC0	%59	220	534
				like protein; similar to	9486.1	36%	529	642
				Z98745 (PID:g2924250)	-)	1	<u>.</u>
CARRET CHAR	1			[Homo sapiens]			_	
HIAHV04	926747	2826	blastx.14	(AC005757) R32611_1	gi 3688089 gb AAC6	100%	3	446
TITA PLINO	11000		1	Homo sapiens	2258.1			
HIAJNUS	750866	5841	HMMER	PFAM: Helicases	PF00271	5.49	20	55

			1.8	conserved C-terminal				
HTDAE43	971582	9597	blastx.14	(AF144054) apoptosis related protein APR-4	gj 4868437 gb AAD3 1316.1 AF144054_1	53%	526	296
HTGCH58	909849	5895	HMMER 2.1.1	Homo sapiens PFAM: RhoGAP domain	PF00620	91.4	420	797
			blastx.14	carboxyl terminus of the predicted protein shows 1 1 comes from this gene;	gi 3874826 emb CAA 86318.1	37% 44% 61%	420 657 771	605 758 809
				cDNA EST EMBL:D32994 comes from this gen				
HTGDM65	967158	5918	blastx.14	SH3 domain binding	gi 1185397 gb AAA8	39%	127	59
				norvegicus]	[//21.1]	39%	186	210
						47%	186	136
						39%	278	210
						28%	337	263
THOTOTI	070710	,				40%	260	195
H1GD191	974962	5921	HMMER 2.1.1	PFAM: SpoU rRNA Methylase family	PF00588	107.6	315	638
			blastx.14	alternate gene name yibK	gi 466744 gb AAB18	100%	315	467
				[Escherichia coli]	583.1	100%	531	638
		_				%92	457	495
CONTOCK	00000					81%	497	529
HIGDW96	96/030	5926	HMMER	PFAM: Domain of unknown function	PF01784	130.2	334	711
			blastx.14	(AL034490) similar to	gi 4008560 emb CAA	%09	1087	1275
				yeast ngg1-interacting	22481.1	43%	460	099
				factor 3		37%	385	513

	 -			[Schizosaccharomyces		61%	361	414
		•		[bombe]		28%	970	1065
				The second distance of the second sec		28%	1312	1347
HTGEL46	685425	5936	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	7.26	398	433
HTGEQ11	967047	5944	HMMER 2.1.1	PFAM: Cytosol aminopeptidase family	PF00883	191	27	305
			blastx.14	aminopeptidase A [Escherichia coli]	gi 1054725 emb CAA 60164.1	95%	320	305
HTGER72	683469	5949	HMMER 1.8	PFAM: Src homology domain 3	PF00018	2.4	174	203
HTGFZ03	923443	2968	HMMER 2.1.1	PFAM: RNA polymerase beta subunit	PF00562	30.7	21	110
	,		blastx.14	(AF025424) RNA polymerase I 127 kDa subunit [Rattus norvegicus]	gi 2739048 gb AAB9 - 4600.1	76%	3	275
HTGGL23	974590	5973	blastx.14	(AE000218) putative adhesion and penetration protein [Escherichia coli]	gi 1787452 gb AAC7 4286.1	87%	(C)	443
HTHCB68	602099	5996	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	3	162	209
HTJAB35	880424	9601	HMMER 1.8	PFAM: Ank repeat	PF00023	35.64	242	325
	948518	9509	blastx.14	(AF182426) arylacetamide deacetylase [Rattus norvegicus]	gi 5923874 gb AAD5 6394.1 AF182426_1	28%	2	160
HTOAK34	008996	6081	HMMER	PFAM: Eukaryotic protein	PF00069	32.41	1020	1190

	1190	0/11			402	399	750	+	33	C.C.	123		140	406	004	538	460	466	460	442	427	481	415	173	157
	954				4	13	235	000	4	-	61		105	200	723	287	278	320	299	287	290	341	287	114	112
	75%				148.5	34%	4 53	?	659	9	7.08		7.82	77	1	%88	20%	53%	42%	42%	43%	40%	46%	10%	%99
	gi 3452473 gb AAC7	1014.1			PF00617	gi 171187 gb AAA34	PF00130		PF00096		PF00049		PF00010	PF00008		gi 3449294 dbj BAA3	2462.1								
kinase domain	(AF084205)	serine/threonine protein	kinase TAO1 [Rattus	norvegicus]	PFAM: RasGEF domain	CDC25 [Saccharomyces kluvveri]	PFAM: Phorbol esters/	diacylglycerol binding	PFAM: Zinc finger, C2H2	type	PFAM:	Insulm/IGF/Kelaxin family	PFAM: Helix-loop-helix DNA-hinding domain	PFAM: EGF-like domain		9.5	[Rattus norvegicus]					_	······································		
1.8	blastx.14				HMMER 2.1.1	blastx.14	HMMER	1.8	HMMER	1.8	HMMER 1 °	1.8	HMMER 1.8	HMMER	2.1.1	blastx.14		***************************************				-			
					6108		6146		6173		6201		6229	6230								,			
					909952		527144		537364		836003		720403	972248	_										
					HTODG16		HTOFT34		HTOHL35		HTOTY09		HTSHF47	HTSHM38											

г																													_	
532	283	280	538	295	544	283	283	286	280	283	283	283	532	535	532	532	304	412	280	286	532	280	283	316	349	268	295	322	283	406
467	245	188	482	245	476	245	188	245	170	230	245	245	485	452	482	482	245	299	251	251	434	245	245	245	317	245	245	251	251	320
20%	61%	35%	47%	52%	39%	61%	31%	20%	73%	25%	%69	53%	20%	35%	47%	47%	20%	31%	10%	28%	30%	28%	53%	37%	63%	75%	47%	37%	54%	31%
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286	460	232	505	376	280	445	268	532	343	262	283	406	505	532	406	379	280	483	268	544	382	376	382	223	235	262	406	409	376	379
230	401	203	473	308	245	329	245	485	251	227	251	296	485	473	344	359	245	454	245	491	320	344	359	203	203	215	359	356	320	320
36%	40%	%09	54%	34%	20%	25%	62%	37%	29%	20%	45%	24%	71%	40%	33%	71%	20%	%09	62%	33%	33%	63%	62%	71%	45%	37%	37%	38%	36%	40%
						_							•																	
																				- U 4444										
																_							•			_				
																														

PFAM: Core histones
_
blastx.14 (AF036548) RGC-32 Raftus norvegicus
HMMER PFAM: Helicases
conserved C-terminal domain
HMMER PFAM: Aldehyde 2.1.1 dehydrogenase family
blastx.14 (AF038838) proline
dehydrogenase [Klebsiella
aerogenes
blastx.14 (AB029335) HrPET-3 [Halocynthia roretzi]

HMMER PFAM: HMG (high 1.8 mobility group) box
HMMER PFAM: Phorbol esters
diacylglycerol binding domain
blastx.14 RAB14 [Rattus
norvegicus
HMMER PFAM: Bacterial mutT protein
HMMER PFAM: Peptidase family 2.1.1

302	700	530	196	143	382	174	247	446	440	158	į	///			421	09	310	885	244	- - 1	521	396	481	487
37.5	555	93	29	6	326	145	170	243	177	8	0,0	956	·		302		170	402	2	l	595	464	537	561
96%	100%	%68	43.1	51%	57%	%09	42%	66	51%	40%	7070	84%			%09	25%	46%	32%	100%))	%88	100%	%89	36%
gi 1763642 gb AAC5	11	gi 5531827 gb AAD4	PF01189	gi 2981631 dbj BAA2	5253.1			PF01131	gi 1742870 dbj BAA1	5551.1	~:147801221_1.1 A A DO	g1 4089132 g0 AAD2	7775.1 AF077042_1		dbj[BAA74972.1		gi 4091782 gb AAC9	9298.1	gi 2330017 gb AAC5	1672.1	gi 4929661 gb AAD3	4091.1 AF151854_1		
mitochondrial intermediate nentidase	precursor [Homo sapiens]	(AF078856) p47 [Homo saniens1	PFAM: NOL1/NOP2/sun family	(AB012223) ORF2 [Canis	familiaris]			PFAM: Prokaryotic DNA topoisomerase	DNA topoisomerase III	(EC 5.99.1) [Escherichia coli]	(AE077042) 20G	(Arru/1042) 303	ribosomal protein S7	nomotog [Homo saptens]	(AB016962) synGAP-b1	[Rattus norvegicus]	(AF051325) SH3 domain	containing adaptor protein	(AF015950) telomerase	reverse transcriptase [Homo sapiens]	(AF151854) CGI-96	protein [Homo sapiens]		
blastx.14		blastx.14	HMMER 2.1.1	blastx.14				HMMER 2.1.1	blastx.14		blocty 14	0145tA.14			blastx.2		blastx.14		blastx.14	***************************************	blastx.14			
		6525	6555	0959				6575			6577	1100			6229		9859		6859		2659			
•		918076	870074	961161				975072			914627	11021			973095		911399		957784		918996			
		HTXNY74	HTXPT68	НТХОС36				HTXRM86			HTXSR88	00000000			HTXSR92		HUJAM39		HUJCM08		HUUAV06			

2.1.1
blastx.14 repressor protein [Homo sapiens]
HMMER PFAM: Phorbol esters and diacylglycerol binding domain
HMMER PFAM: Bacterial mutT protein
blastx.14 (AL033536) predicted
using Genefinder; similar to 1 1 elegans
HMMER PFAM: Lectin C-type
domain short and long forms
blastx.2 (AF175206) lectin-like receptor F1 [Homo sapiens]
HMMER PFAM: Zinc finger, C2H2 1.8 type
HMMER PFAM: Peptidase family 2.1.1
blastx.2 (AF106037) adipocytederived leucine aminopeptidase [Homo saniens]
blastx.14 Zn-binding protein [Pleurodeles walt]
HMMER PFAM: Plexin repeat

283	471 396	583	343	412	1198	1798	484	510		424	· !	868			205		766	1040	863	336		434	306	270	156	7	69	118
215	409 295	1215	513	642	1272	1824	278	487		531	 ! !	857			185		806	066	837	184		273	217	172	203	84	125	150
34%	42%	62%	%99	45%	44%	%99	63%	75%		100%		4.8			4.15		83%	100%	%88	38.64		81%	%96	36%	62%	34%	36%	63%
gi 1196433 gb AAA8 8038.1		gi 709961 gb AAC52	167.1				gi 5020264 gb AAD3	8043.1 AF151363_1		gi 4929707 gb AAD3	4114.1 AF151877 1	PF00076			PF00099		gi 5441611 emb CAB	46854.1		PF00010		gi 4689256 gb AAD2	7831.1[AF121858_1		gi 334072 gb AAA47	471.1		
unknown protein [Homo sapiens]		retinoid X receptor	interacting protein [Mus	musculus]			(AF151363) Cdc42	GTPase-activating protein	[Mus musculus]	(AF151877) CGI-119	protein [Homo sapiens]	PFAM: RNA recognition	motif. (aka RRM, RBD,	or RNP domain)	PFAM: Zinc-binding	metalloprotease domain	(AJ388555) hypothetical	protein [Canis familiaris]		PFAM: Helix-loop-helix	A T1916.60	(AF121858) sorting nexin	8 [Homo sapiens]		ORF-3 protein	[Pseudorabies virus]		
blastx.14		blastx.14	,				blastx.14			blastx.14		HMMER	1.8		HMMER	1.8	blastx.14			HMMER 18	1.1	blastx.14			blastx.14			
6711		6714		_		1	6715	_		6720		6722			6741		6771		1	6785	0007	0789			6831			
929586		960646		· 		1	299606			959449		868363	_		747723		963498			685289	015050	050516			926017			,
HWAGX37	3	HWAHI10			•	1 Oct 1 titl	HWAHS94	_		HWBAL44		HWBAQ16			HWBBR65		HWBDM24		Pozer dirri	HWBEX2/	HVAAF22	n i AAr53		0000	HYAASU8			

211	427	27	36	112	591	688	297	420	684	142	654	388	562				464	·····		17	142	200	_ nnc
282	257	206	263	2	505	869	382	103	604	7	619	263	2		_	-	141			112	195	398	707
37%	27.8	6.06	%19	47	33.3	71%	29%	46%	10%	48%	%99	32.5	92%				34%			34%	20%	28%	4070
	PF00047	PF00207	gb AAA39508.1	PF00617	PF00036	gi 4038292 gb AAC9	7349.1		-			PF00643	gi 4325109 gb AAD1	7259.1			emb CAA97423.1			gi 5305335 gb AAD4	1594.1 AF071081_1		
	PFAM: Immunoglobulin domain	PFAM: Alpha-2- macroglobulin family	alpha-2-macroglobulin [Mus musculus]	PFAM: RasGEF domain	PFAM: EF hand	(AF106071) ras activator	RasGRP [Homo sapiens]					PFAM: B-box zinc finger.	(AF119043)	transcriptional	intermediary factor l	gamma, 111 gamma [Homo sapiens]	predicted using	Genefinder	[Caenorhabditis elegans]	(AF071081) proline-rich	mucin homolog	[Mycobacterium	[uocivara]
	HMMER 2.1.1	HMMER 2.1.1	blastx.2	HMMER 2.1.1	HMMER 2.1.1	blastx.14						HMMER 2.1.1	blastx.14				blastx.2			blastx.14			
	6848	0989		£989	6883							2689					6918			6934			
	971448	900008		956606	862606							909031					944080			509696			
	HYABP53	HYABB43		HYAAU65	HWBEG18							HWBCS08					HWBAQ71			HWAFG12			

Q. O	34% 219 142 44% 154 101 32% 374 300 34% 365 297 34% 332 264 63% 338 306 29% 365 294 38% 314 261	208 178 253 78 93 249 221 240 237	25% 248 23.2 40 446948.1 55% 7 59% 169 60% 400 38% 346	147.95 116 147.95 116 42000.1 98% 86
6948		(AF010144) neuronal thread protein AD7c-NTP [Homo sapiens]	PFAM: Immunoglobulin domain CMRF-35 antigen [Homo sapiens]	PFAM: Ras family (contains ATP/GTP binding P-loop) rab-related GTP-binding
IWAFA47 HWAEG71		6938	887166 6942	6946

	215	209	452	209	308	552		381		480	550	594	578	616	417	250	187	119	231	226	196	199	149	117	149	126
	3	12	381	18	228	280		19		29	2	571	552	296	770	417	300	226	278	261	261	258	181	152	229	152
	29.5	%69	%02	31%	29%	96		225.7		91%	82%	100%	77%	100%	%66	%68	71%	28%	87%	100%	54%	%09	81%	83%	40%	100%
	PF00435	gi 5262574 emb CAB	45729.1			PF01163		PF01182		emb CAA03416.1	gi 4826478 emb CAB	42896.1			gi 4959568 gb AAD3	4394.1 AF132984_1					7. 7.					***************************************
norvegicus]	PFAM: Spectrin repeat	(AL080133) hypothetical	protein [Homo sapiens]			PFAM:	RIO1/ZK632.3/MJ0444 family	PFAM: Glucosamine-6-	phosphate isomerase	unnamed protein product [unidentified]	similar to SH3-binding	protein [Homo sapiens]			(AF132984) nuclear pore	complex interacting	protein NPIP [Homo	sapiens]								
	HMMER 2.1.1	blastx.14				HMMER	2.1.1	HMMER	2.1.1	blastx.2	blastx.14				blastx.14						**************************************					
	6947					9569		6971			6984				9869											
	958115					756888		949088			944903				940813											
	HWAEC08		-			HWACY70		HWABG11			HUUDR34				HUUCJ02											

						%99	300	274
HTX0015	869261	7011	HMMER 2.1.1	PFAM: Ubiquitin family	PF00240	44.9	130	273
HTXLS08	958357	7023	blastx.14	(AF090989) high-risk	gi 4151328 gb AAD1	48%	745	786
				human papilloma viruses	2543.1	%89	1006	1146
				E6 1 alpha [Homo		41%		237
			,	sapiens]		21%	511	645
					,	10%	427	477
						27%	580	645
HTWKB07	952841	7085	blastx.14	(AF003535) ORF2-like	gi[2197085[gb[AAD0	%09	. 25	84
				protein [Homo sapiens]	4635.1	75%	259	294
						20%	205	258
						33%	36	116
				,		%0/	167	196
HTWJH08	790185	7087	blastx.2	(AK000385) unnamed	dbj BAA91131.1	61%	197	51
				protein product [Homo sapiens]				
HTWJH08	846554	9615	blastx.2	(AK000385) unnamed	dbj BAA91131.1	61%	197	51
				protein product [monito sapiens]				
HTWJF50	911448	6802	blastx.14	myosin I [Rattus	gi 3724141 emb CAA	48%	1009	1428
				norvegicus]	50871.1	23%	334	681
						25%	732	851
						46%	863	1012
						39%	40	108
						20%	989	715
ні мғQ19	586124	7091	HMMER 2.1.1	PFAM: Sema domain	PF01403	62.9	14	184
HTOIA82	844319	7198	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	4.25	50	82
HTOHI14	659280	7204	HMMER	PFAM: Asparaginase	PF01112	20.7	140	217

			2.1.1					
НТОРМ08	960113	7222	blastx.14	(AF106069) deubiquitinating enzyme [Homo sapiens]	gi 5814097 gb AAD5 2099.1 AF106069_1	33%	5	367
HTHBY73	946168	7282	blastx.2	(AK001868) unnamed protein product [Homo sapiens]	dbj BAA91951.1	52% 45%	162	183
HTGEX10	963862	7305	HMMER 2.1.1	PFAM: SET domain	PF00856	105.2	580	096
			blastx.14	(AC005065) determined by GENSCAN prediction and 1	gi 4153862 gb AAD0 4721.1	65%	601	1017
HTGEA37	909806	7311	blastx.14	(AF001293) aiolos [Mus musculus]	gi 2150044 gb AAB5 8795.1	%08		216
HTAIF22	910040	7364	HMMER 2.1.1	PFAM: RhoGEF domain	PF00621	29.5	320	394
			blastx.14	(AL022271) similar to Guanine nucleotide exchange 1 1 1 this g	gi 3876654 emb CAA 18349.1	64%	281	397
HTAIF11	965738	7365	blastx.14	(AF061555) ubiquitin- protein ligase E3-alpha [Mus musculus]	gi 3170887 gb AAC4 0165.1	48%	6 297	293 392
HTAEV23	959129	6982	HMMER 2.1.1	PFAM: WW domain	PF00397	25.9	478	386
			blastx.14	This gene is novel. [Homo sapiens]	gi 603953 dbj BAA07 893.1	%68	823	359
HTAEP05	932459	7370	blastx.14	Pro-Pol-dUTPase polyprotein [Mus	gi 2065210 emb CAA 73251.1	76%	225 406	275
				ınuscunusj		47%	500	59 553

412	430	492		287	000	302		299	152	484		-	511		505	618		82	131	207	257	304	285	349
386	371	448		123		102		. 135	24	176		•	233		236	502		5	57	133	219	260	52	287
77%	23.3	7.29	-	%86	, ,	45.3		83%	%09	%19			58.09		61%	52%		46%	40%	36%	61%	46%	979	%9 <i>L</i>
	PF01360	PF00369		gi 5817084 emb CAB	33/09.1 DE00607	FFU00U/		gi 1780975 emb CAA	71418.1	dbj BAA91205.1			PF00001		gb AAC64595.1			gi 1196431 gb AAA8	8036.1				dbj BAA91131.1	
	PFAM: Monooxygenase	PFAM: Hvdroxvmethvlølntarvl-	coenzyme A reductase	(AL110271) hypothetical	DEAM: 629 Gene protein	p24 (core nucleocapsid	protein)	gag protein [Human	endogenous retrovirus K]	(AK000496) unnamed	protein product [Homo	sapiens	PFAM: 7 transmembrane	receptor (rhodopsin family)	(AF091575) olfactory	receptor [Rattus	norvegicus	unknown protein [Homo	sapiens]				(AK000385) unnamed	protein product [Homo sapiens]
	HMMER 2.1.1	HMMER 1.8		blastx.14	HWWEB	2.1.1		blastx.14		blastx.2			HMMER	1.8	blastx.2			blastx.14					blastx.2	
	7379	7408		7458	7504	F 0			}	7551			7554					7581					7603	
	720684	940661		959943	908440			4 ————		948720			928378					915363					743400	
	HTABK47	HSYCV01		HSAWR08	HSAIII.84					HNHOF94			HNHNP81					HNHLC01					HNHGV62	

HNHGE31	698046	7624	HMMER	PFAM: Zinc-binding	PF00099	3.3	83	109
			1.8	metalloprotease domain				
HNHFV49	975415	7644	blastx.2	hypothetical protein (L1H	pir B34087 B34087	81%	483	190
				3' region) - human		71%	227	9
						%06	217	188
HNHFH24	903741	7657	HMMER	PFAM:	PF00209	37.2	208	306
			2.1.1	Sodium:neurotransmitter				
				symporter family				
			blastx.14	(AF075266) orphan	gi 3347930 gb AAC2	%9L	187	327
				transporter isoform B9	7761.1	27%	414	467
				[Mus musculus]				***************************************
HNHDF07	953883	7702	HMMER	PFAM: Fibronectin type	PF00041	7.48	242	319
			1.0	III domain				
HNHDC29	904546	7704	blastx.14	contactin associated	gi 1857708 gb AAB4 8481 11	%86	219	7
HNHCI32	861673	7716	HMMFR	PFAM: 7 transmembrane	DEOUDO1	122 17	105	545
))	1.8	recentor (rhodonein	100001	11.001	193	C+C
		_	2	family)				
		_	blastx.2	(AF112461) G protein-	gb AAF27279.1 AF1	100%	189	551
				coupled receptor 57	12461_1	100%	112	186
				[Homo sapiens]	•	100%	26	112
HNHCI32	956105	9645	HMMER	PFAM: 7 transmembrane	PF00001	133.17	951	601
			1.8	receptor (rhodopsin				
		a		family)	:	.,		
			blastx.2	(AF112461) G protein-	gb AAF27279.1 AF1	100%	555	917
				coupled receptor 57	12461_1	100%	478	552
				[Homo sapiens]		100%	422	478
HNHBF47	949027	7731	HMMER	PFAM: Cadherin	PF00028	44.76	899	522
			1.8					
			blastx.2	(AB028499) Flamingo 1	dbj BAA84070.1	%96	409	999

259	923	398	099	099	099	968	669	884	068	247	253	648	235	884	247	247	878	669	854	708	380	380	398	371	371	362	829	262	764	374
5	999	243	412	370	412	699	355	999	648	70		361	14	654	14	26	999	412	672	433	270	270	270	270	270	264	683	2	723	270
92%	%16	%98	42%	36%	36%	43%	33%	43%	39%	38%	32%	30%	36%	39%	37%	35%	35%	32%	37%	78%	40%	35%	37%	44%	38%	33%	32%	78%	57%	35%
																														
				_	•••																			·						
ulus]																														
[Mus musculus]																														
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HNHAF61 955094	7745	HMMER 1.8 blastx.2 blastx 14	PFAM: Cadherin	PF00028	46.67	330	161
	9649	blastx.2)	401
	9649	blasty 14	(AF152473)	gb AAD43734.1 AF1	75%	81	677
	9649	blasty 14	protocadherin alpha C1	52473_1	84%	173	364
	9649	hlasty 14	short form protein [Homo		33%	87	989
	9649	hlasty 14	sapiens]		93%	<u> </u>	84
	9649	hlasty 14			40%	10	75
		Olumbra, 1	(AF152303)	gi 5456892 gb AAD4	%86	325	1071
	,		protocadherin alpha C1	3697.1	40%	715	186
			[Homo sapiens]		42%	499	099
					32%	778	1023
					37%	724	867
					100%	225	275
					17%	176	229
				-	30%	496	684
erid des					%68	569	325
					35%	895	1011
					40%	268	693
					36%	717	791
					20%	499	540
HNGOZ40 969158	7757	blastx.14	(AF155098) NY-REN-8	gi 5360091 gb AAD4 (78%	299	477
	\neg		antigen [Homo sapiens]	2864.1 AF155098_1			
HNGNY02 918626	6977	HMMER	PFAM: FAD/NAD-	PF00175	4.43	366	440
		7.8	onding domain in oxidoreductases				
HNGND01 915294	8777	HMMER	PFAM: Phorbol esters/	PF00130	2.07	464	490
		 8.	diacylglycerol binding domain				·
HNGMW65 950173	7781	blastx.2	(AF010144) neuronal	gb AAC08737.1	62%	340	143
			thread protein AD7c-NTP	- · ·	%19	340	248

247	247	3	25	111	346	152	351	125	18	349	392	1		77	7	42	210	526		817	2	2	2	2	2	2	2	<u>~</u>
417	345	80	81	200	414	205	392	202	98	269	219			199	43	11	242	437		7	196	193	199	196	193	199	193	196
45%	%09	25%	%89	43%	43%	55%	64%	21%	47%	6.93	79%			41%	71%	83%	72%	5.95		40%	61%	62%	54%	52%	54%	53%	20%	44%
										PF00031	gi 4186073 emb CAA	09423.1		sp Q29386 Q29386				PF00505		emb CAB55945.1	gi 506502 emb CAA5	6225.1						
[Homo sapiens]										PFAM: Cystatin domain	(AJ010949) calcium	channel alpha-2-delta-C	subunit [Mus musculus]	KERATIN TYPE II	CYTOSKELETAL 8	(FRAGMENT).		PFAM: HMG (high	A 117 GOUD) DOA	(ALTI/4/0) hypothetical protein [Homo sapiens]	NK10 [Mus musculus]							
							•			HMMER 1.8	blastx.14			blastx.14				HMMER 18	1.1	blastx.2	blastx.14							
										7788	7791			7795				7801			7837							
										974358	948825			952236				942758			964715			,				
	*									HNGMD48	HNGLY08			HNGLL07				HNGKM74	_		HNGIR10							

2	92	83	П	2	2	104	197	256	238	130	921	466)	385	520	283	214	317	152	368	292	205	104	82	284	320	19
193	199	196	178	217	115	181	232	309	306	285	986	290		287	404	230	140	258	39	324	381	276	154	210	261	391	93
45%	61%	57%	37%	76%	39%	46%	20%	33%	30%	78%	%98	33.71		54%	41%	77%	36%	%01	42%	53%	36%	20%	47%	20%	5.01	45%	40%
										gi 4186073 emb CAA	.09423.1	PF00047		gb AAD34946.1 AF1	43185_1			gi 509838 gb AAA87	332.1		gi 439877 gb AAB02	291.1			PF00098	gi 2072966 gb AAC5	1272.1
										(AJ010949) calcium	channel alpha-2-delta-C subunit [Mus musculus]	PFAM: IG	(immunoglobulin) superfamily	(AF143185) high affinity	immunoglobulin gamma	Fc 1		pol polyprotein [Baboon	endogenous virus]		reverse transcriptase	[Homo sapiens]			PFAM: Zinc finger, CCHC class	p40 [Homo sapiens]	
										blastx.14		HMMER	1.8	blastx				blastx.14			blastx.14				HMMER 1.8	blastx.14	
										7879		7897						7902			7933				7952	7973	
				_						941480		951489						967314			967512				959964	959977	
	·····			-						HNGFF50		HNGEO79						HNGEI11			HNGDM11				HNGDA08	HNGAZ08	

100	792	115	150	64	91	91	91	232	44	316	340	125	307	6	113		200	518	909	594	403	131	244
144	316	14	200	384	387	420	339	387	79	405	360	18	68	88	51		24	3	550	550	281	48	134
40%	35%	100%	2.96	%06	44%	42%	38%	44%	100%	27%	85%	40.5	84%	100%	27 49		32.11	78%	63%	53%	36%	46%	35%
		gi 4680667 gb AAD2 7723.1 AF132948_1	PF00047	gi 3894323 dbj BAA3	4639.1							PF00797	gi 2624972 gb AAB9	4880.1	PF00335		PF00240	gi 5733824 gb AAD4	9751.1 AF176069 1	1	gi 53669 emb CAA37	876.1	
		(AF132948) CGI-14 protein [Homo sapiens]	PFAM: IG (immunoglobulin) superfamily	(AB020063) Keap1 [Mus	musculus]							PFAM: N- acetyltransferase	(AF020313) proline-rich	protein 48 [Mus	PFAM: 4 transmembrane	segments integral membrane proteins	PFAM: Ubiquitin family	(AF176069) ubiquilin	[Homo sapiens]		decorin (PGII) [Mus	musculus]	
		blastx.14	HMMER 1.8	blastx.14								HMMER 2.1.1	blastx.14		HMMER	1.8	HMMER 1.8	blastx.14			blastx.14		
		7997	8003	8051								8067	8125		8141	 	8184				8196		
		966347	733297	955894								529571	909931		893995		927097				921263		
!		HNFID11	HNFHR56	HNEDO77								HNEBJ81	HMWEN61		HMWBT59		HMSMN71				HMSJL53		

HMSHE81	784966	8218	HMMER 2.1.1	PFAM: PX domain	PF00787	29.1	128	421
HMSDL70	909997	8240	blastx.14	(AF083331) kinesin-like protein KIF1B [Rattus norvegicus]	gi 3493139 gb AAC3 3292.1	100%	2	103
HMSBO95	796724	8258	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.61	273	302
HMMBL55	731523	8320	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.03	227	271
HMMAT08	929005	8327	blastx.14	DOCK180 protein [Homo sapiens]	gi 1339910 dbj BAA0 9454.1	49%	137	301
HMCHZ77	771795	8350	HMMER 2.1.1	PFAM: Nucleoside transporter	PF01733	81.6	5	283
HMALZ77	856266	8362	HMMER 2.1.1	PFAM: Isochorismatase family	PF00857	88.5	2	232
HMAJL09	950168	8365	HMMER 1.8	PFAM: ADP-glucose pyrophosphorylase	PF00483	150.92	20	256
			blastx.14	f270 [Escherichia coli]	gi 290545 gb AAA62 048.1	100%	254	469
HMAIQ20	669436	8367	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	3.43	172	234
HMAIH15	956705	8368	blastx.2	Hypothetical protein MJ0456 [Escherichia coli]	dbj BAA35499.1	100%	3	203
HMAIA55	899404	8369	blastx.2	(AF027204) putative tetraspan transmembrane protein L6H [Homo sapiens]	gb AAB82947.1	35%	188	532
HMADF74	944465	8377	HMMER 2.1.1	PFAM: Leucine Rich Repeat	PF00560	42.8	369	440

			blastx.2	leucine-rich repeat protein	emb CAA76000.1	34%	294	674
				[Arabidopsis thaliana]				
HMACV54	922354	8379	HMMER	PFAM: Aldose 1-	PF01263 ·	116	418	176
	, 10000	1,000	4.1.1	epinierase				
HMABD66	388074	8381	HMMER 2.1.1	PFAM: 60Kd inner membrane protein	PF02096	59.8	. 222	365
HLYHK61	932994	9888	blastx.14	GTP binding protein [Mus	gi 53169 emb CAA36	%88	133	420
	-			[musculus]	803.1	%56	489	989
	-					%96	33	131
					-	82%	723	809
	1					%06	398	487
HLYHK34	703776	8387	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	13.18	436	519
HLYGQ11	966539	8401	HMMER	PFAM: RNA recognition	PF00076	4.45	96	134
			1.8	motif. (aka RRM, RBD, or RNP domain)				-
HLYEA70	943886	8431	HMMER	PFAM:	PF00701	22.8	304	408
			2.1.1	Dihydrodipicolinate) } -
				synthetase family				
HL YCF37	949401	8459	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	12.84	1249	1326
HLYBX91	790234	8463	HMMER	PFAM: Zinc-binding	PF00099	3.14	710	754
			1.8	metalloprotease domain				
HLMHL66	910804	8555	HMMER	PFAM: Fibrinogen beta	PF00147	40.5	157	252
			2.1.1	and gamma chains, C-] }
***				terminal globular domain				
			blastx.14	(AF107253) angiopoietin	gi 4378598 gb AAD1	92%	157	252
				Y1 [Homo sapiens]	9608.1	72%	333	365
,		3				30%	41	100
HLCDA67	88/3/5	8581	HMMER	PFAM: BTB/POZ domain	PF00651	101.9	160	504

	146	212	206	200	206	206	212	233	212	191	212	206	191	212	212	149	149	161	212	149	234	234	234	234	234	234	234	234	234
	78	3	3	3	3	9	6	33	18	3	21	3	21	3	12	3	3	9	69	3	166	172	172	172	181	181	181	154	181
	39.9	62%	64%	29%	54%	%95	47%	45%	43%	49%	40%	38%	43%	40%	43%	42%	42%	48%	37%	36%	39%	47%	38%	33%	44%	20%	55%	25%	20%
	PF00096	gb AAB97932.1																									_		
	PFAM: Zinc finger, C2H2 type	(AC004076) R30217_1	[Homo sapiens]														***************************************												
2.1.1	HMMER 2.1.1	blastx.2																									W. T. August		
	0098																			·									
	909242																												
	HJPAY56																												

	••••					77%	208	234
						44%	181	234
						55%	208	234
						46%	190	234
HJPAA60	586675	8604	HMMER 2.1.1	PFAM: Adenosine/AMP deaminase	PF00962	78.6	96	533
HJBCZ05	925805	8611	HMMER 1.8	PFAM: TPR Domain	PF00515	12.67	205	291
			blastx.14	(AF132856) suppressor of	gi 4809026 gb AAD3	%88	520	840
	·			G2 allele of skp1 homolog	0062.1	%86	85	357
				[Homo sapiens]		28%	262	698
						25%	151	258
HHEZO92	942859	8638	HMMER 2.1.1	PFAM: tRNA synthetase class II (G, H, P, S and T)	PF00587	59.7	94	450
			blastx.14	(AC002131) Similar to	gi 3157938 gb AAC1	62%	97	306
				seryl-tRNA synthetase 1	7621.1	47%	325	507
				[Arabidopsis thaliana]				
HHEWX06	933879	8643	blastx.14	ORF 3 [Rattus	gi[57053 emb CAA29	32%	38	241
				norvegicus	033.1	53%	5	43
HHEPG59	925436	8681	blastx.14	IP63 protein [Rattus	gi 2764951 emb CAA	28%	251	99
				norvegicus]	67705.1	52%	541	440
						20%	346	257
HHEMG02	917366	8704	blastx.14	similar to NIFS protein	gi/722379 gb AAC46	%19	525	809
				(nitrogen fixation)	685.1	%95	441	488
				[Caenorhabditis elegans]		53%	641	685
HHELA35	878217	8711	HMMER 2.1.1	PFAM: Beta-lactamase	PF00144	175.4	118	450
HHEKZ12	878267	8712	HMMER 1.8	PFAM: Beta-lactamases	PF00144	132.1	102	380
HHEAJ78	773538	8739	HMMER	PFAM: Helicases	PF00271	3.92	2	82
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blastx.14 The hal 438 gene product
is related to a C728
protein 1
HMMER PFAM: Helicases
1.8 conserved C-terminal domain
HMMER PFAM: FAD binding 2.1.1 domain
blastx.2 Aip2p [Saccharomyces
cerevisiae
HMMER PFAM: Fibronectin type 2.1.1 III domain
blastx.2 (AF117210) host cell
factor 2 [Homo sapiens]
_
HMMER PFAM: Core histones 1.8 H2A, H2B, H3 and H4
blastx.14 alpha-3 type IX collagen
[Homo sapiens]

1
blastx.14 polyprotein [Hepatitis C
virus]
blastx.14 (AL021749) protein
phosphatase 2C-like
protein [Arabidopsis
thaliana
HMMER PFAM: WD domain, G-
2.1.1 beta repeat
blastx.14 (AF072880) SOCS box-
containing WD protein
7
blastx.14 (AF151872) CGI-114
HMMER PFAM: ATP synthase A
_
HMMER PFAM: Zinc-binding
1.8 metalloprotease domain
blastx.14 (AL117483) hypothetical

542	105	167	1004	<i>L</i> 99	1408		1408		146		1067		1070		135		252			410		263	377	377	553	553
453	4	105	615	278	1331	1 1 1	1331		66		1783		1723		19					144		192	12	12	335	335
46%	35%	42%	53.09	53.23	12.8		12.8		4.29		197.8		%99		32.9		61%			%86		52.4	40%	36%	46%	47%
55956.1			PF00054	PF00054	PF00125		PF00125		PF00099		PF00632		pir B38919 B38919		PF00096		gb AAD22522.1 AF0	91457_1		gi 4206088 gb AAD1	1417.1	PF00096	gb AAC50252.1			
protein [Homo sapiens]			PFAM: Laminin G domain	PFAM: Laminin G	PFAM: Core histones	H2A, H2B, H3 and H4	PFAM: Core histones	H2A, H2B, H3 and H4	PFAM: Zinc-binding	metalloprotease domain	PFAM: HECT-domain	(ubiquitin-transferase).	hypothetical protein 2 -	numan (tragment)	PFAM: Zinc finger, C2H2	type	(AF091457) zinc finger	protein RIN ZF [Rattus	norvegicus]	(AF086837) snapin	[Homo sapiens]	PFAM: Zinc finger, C2H2 type	zinc finger protein	ZNF132 [Homo sapiens]		
			HMMER 1.8	HMIMER 1.8	HMMER	1.8	HMMER	1.8	HMMER	1.8	HMMER	2.1.1	blastx.14		HMMER	2.1.1	blastx.2			blastx.14		HMMER 2.1.1	blastx.2			
			8860	9731	8871		9732		6688		8916				8928			_		8932		8934				
_			899636	902517	937609		941948		915919		957580				961309					914667		909040		-		
			HDTBD67	HDTBD67	HDTAA31		HDTAA31		HDPXN01		HDPUN39				HDPSB10					HDPRR24		HDPRJ04				

∞	7	7	4	7	4	7		_	3	_	4	_	3	_	<u>~</u>				_	_	_	_	_	_						
53	37	37	57	37	57	37	538	37	55	37	57.	37	55	37	53	55	37	37	55.	57	517	37	553	538	37	192	61]	61]	611	611
335	18	12	335	12	335	12	335	12	335	12	335	12	335	12	380	326	12	39	335	380	335	12	380	380	93	51	513	570	534	573
47%	35%	34%	41%	34%	38%	31%	44%	28%	43%	30%	37%	31%	41%	31%	46%	36%	78%	30%	36%	35%	37%	27%	34%	33%	79%	33%	36%	20%	30%	%69
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611	611	611	611	599	365	611	354	611	371	976	576	490	646	582	187	83	700	774	788	746	100	/6/	411	226				445
534	573	573	582	513	303	513	292	573	327	544	544	200	530	523	155	700	771	803	823	417		414	262	366	•			287
30%	46%	46%	%09	27%	34%	30%	45%	46%	40%	45%	45%	42%	41%	%09	54%	85%	54%	100%	%99	102.12	7000	/8//	9.7%	87%				57.51
												gi 5080816 gb AAD3	9325.1 AC007258_14			pir JE0363 JE0363				PF00065	4b:1D A A 00222 11	doj DAA09322.1		gi 3694664 gb AAC6 2434.1				PF00433
									,			(AC007258) Putative	ATPase [Arabidopsis	thaliana]		mitogen-activated protein	kinase kinase kinase (EC	2.7) 1		PFAM: Neurotransmitter-	GABA recentor who 3	Cithinit programme [Dotter	subulity preductor [Kallus norvegicus]	(AC004893) similar to NEDD-4 (KIA0093);	similar to P46934	(PID:g1171682) [Homo	sapiens]	PFAM: Protein kinase C
												blastx.14				blastx.14				HMMER 18	hlastx	V Chr		blastx.14	_			HMMER
					_							8939				8941				6568				6868				8991
					···							922006			,	923120				973945				921381				909833
			- 11.								0)104411	HDPQ168				HDPQF03		-		HDPL162				HDPGS45	•			HDPGS16

			1.8	terminal domain				
	******		blastx.2	(AJ245709) Akt-3 protein	emblCAB53537 11	100%	226	037
				[Homo sapiens]		100%	3	116
HDPFZ70	709684	9003	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	13.5	662	745
HDPFB03	936331	9015	blastx.14	(AF043726) PHD-finger protein [Mus musculus]	gi 4529845 gb AAD2	38%	341	553
HDPDD12	970592	9017	blastx.14	(AF000998) CLOCK [Mus musculus]	gi 2114488 gb AAC5	%98	284	370
HDPCM62	454740	9031	HMMER 1.8	PFAM: Laminin B (Domain IV)	PF00052	2.03	152	208
HCWKR86	784705	6806	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.26	296	340
HCWFA35	908820	9114	HMMER 1.8	PFAM: DnaJ, prokaryotic heat shock protein	PF00226	116.61	80	274
			blastx.14	Curved DNA-binding protein cbpA [Escherichia coli]	gi 1651491 dbj BAA3 6142.1	%86	89	364
HCUGN19	716989	9181	HMMER 1.8	PFAM: Alcohol/other dehydrogenases, short chain type	PF00106	8.05	86	151
HCUGL20	668913	9184	HMMER 1.8	PFAM: Ank repeat	PF00023	7.2	190	261
HCFNG10	848225	9310	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	6.03	305	376
HCFMZ90	922112	9315	HMMER 1.8	PFAM: Beta-ketoacyl synthases	PF00109	194.57	291	872
			blastx.14	(AF021234) 3-oxoacyl- [acyl-carrier-protein]-	gi 2522482 gb AAB8 1078.1	57%	465	824 494
				symmas [Montospora		41%	91	306

				crassal				
HCFMW71	920506	9316	HMMER 2.1.1	PFAM: Isopentenyl-diphosphate delta-	PF01772	55.5	198	362
			blastx.14	homologue of yeast IPP	gi 488750 emb CAA3	42%	198	407
HCFMJ37	955281	9321	blastx.2	(AF161445) HSPC327	9590.1 05 A A F 2 9 0 0 5 1 A E 1	0/70	500	199
				[Homo sapiens]	61445_1	%56	203	010
1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2					1	100%	610	654
HCFCG23	850426	9337	HMMER	PFAM: Core histones	PF00125	10.89	179	244
HBTAE84	781946	9355	HMMER	PFAM: ATPases	PF00004	20.81	122	232
_			1.8	associated with various			1	707
HRMTR85	023730	0300	14 14 14	(A FOOT 402)				
	06/676	0666	olastx.14	(AF 093403) 2-amino-3-	gl4093159[gb]AAC9	93%	3	182
				ketobutyrate-coenzyme A	9774.1	100%	261	317
				ligase [Mus musculus]		100%	217	258
HBMBF89 	912789	9415	blastx.14	Rab24 protein [Mus	gi 438164 emb CAA8	95%	287	412
ראמואו מזו	70000	2070	40 0 41	chiuchii	04/2.1	89%	96	152
	7.20475	9423	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding	PF00130	3.77	193	252
				domain				
HBJLR37	849633	9437	HMMER	PFAM: Ribosomal protein	PF01283	232.2	2	325
			2.1.1	S26e				
HBJLR31	88006	9438	HMMER	PFAM: Zinc finger, C2H2	PF00096	06	861	998
			2.1.1	type				
			blastx.2	(AF185576) POZ/zinc	gb AAF03152.1 AF1	%89	909	953
				finger transcription factor	85576_1	33%	618	893
TIDITYES	000000	0,1		ODA-8 Mus musculus		36%	99	185
HBJJXJ3	835/33	9452	HMMER	PFAM: IG	PF00047	9.2	157	207

			1.8	(immunoglobulin)				
		···········		superfamily		_		
····			blastx.2	(AF161081) activatory	gb AAD52965.1 AF1	%06	157	216
				receptor PIRIIbeta [Homo	61081_1	73%	215	283
TIPITETO	27.07.00			sapiens				
HBJJ112	894345	9453	HMMER	PFAM: Homeobox	PF00046	64	201	371
1111 11170	0000		2.1.1	domain				
HBJIH60	930448	946]	HMMER	PFAM: Laminin B	PF00052	1.57	181	204
			1.8	(Domain IV)				
HBJHX73	971377	9466	HMMER	PFAM: Laminin G	PF00054	13.48	931	1005
		·	1.8	domain			1))
			blastx.14	contactin associated	gi 1857708 gb AAB4	20%	451	876
		···		protein [Homo sapiens]	8481.1	29%	880	975
						33%	349	447
						42%	985	1041
COTOTATI		1				43%	916	963
HBJU103	923800	9472	HMMER 1.8	PFAM: Cyclic nucleotide- binding domain	PF00027	8.96	41	100
HBJFC23	423885	9484	HMMER	PFAM: WD domain, G-	PF00400	32.1	135	251
			2.1.1	beta repeat				
HBJAB15	660552	9522	HMMER	PFAM: Phorbol esters /	PF00130	2.72	145	171
			1.8	diacylglycerol binding domain				
HBDAD64	864344	9524	HIMMER	PFAM: Zinc-binding	PF00099	3.09	423	443
			1.8	metalloprotease domain		_)
HBCCJ05	930956	9527	blastx.14	(AF164612) Gag protein	gi 5802816 gb AAD5	48%	444	277
				[Homo sapiens]	1794.1 AF164612 1	47%	536	486
HBCBN51	952057	9532	HMMER	PFAM: alpha/beta	PF00561	43.4	358	564
			2.1.1	hydrolase fold		_		
			blastx.14	similar to alpha/beta	gi 3878848 emb CAB	40%	741	1007
								- , , ,

	429	69	525	717	643
	358	7	478	859	571
	28%	57%	62%	45%	701/5
	03219.1				
	hydrolase fold; cDNA	EST 1			

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_					

[053] Table 2 further characterizes certain encoded polypeptides of the invention, by providing the results of comparisons to protein and protein family databases. The first column provides a unique clone identifier, "Clone ID NO:", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig indentifier. "Contig ID:" which allows correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide The fourth column provides the analysis method by which the sequences. homology/identity disclosed in the row was determined. The fifth column provides a description of PFam/NR hits having significant matches identified by each analysis. Column six provides the accession number of the PFam/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in column five. Comparisons were made between polypeptides encoded by polynucleotides of the invention and a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFam"), as described below.

The NR database, which comprises the NBRF PIR database, the NCBI [054] GenPept database, and the SIB SwissProt and TrEMBL databases, was made nonredundant using the computer program nrdb2 (Warren Gish, Washington University in Saint Louis). Each of the polynucleotides shown in Table 1A, column 3 (e.g., SEQ ID NO:X or the 'Query' sequence) was used to search against the NR database. The computer program BLASTX was used to compare a 6-frame translation of the Query sequence to the NR database (for information about the BLASTX algorithm please see Altshul et al., J. Mol. Biol. 215:403-410 (1990), and Gish et al., Nat. Genet. 3:266-272 (1993)). A description of the sequence that is most similar to the Query sequence (the highest scoring 'Subject') is shown in column five of Table 2 and the database accession number for that sequence is provided in column six. The highest scoring 'Subject' is reported in Table 2 if (a) the estimated probability that the match occurred by chance alone is less than 1.0e-07, and (b) the match was not to a known repetitive element. BLASTX returns alignments of short polypeptide segments of the Query and Subject sequences which share a high degree of similarity; these segments are known as High-Scoring Segment Pairs or HSPs. Table 2 reports the degree of similarity between the Query and the Subject for each HSP as a percent identity in Column 7. The percent

identity is determined by dividing the number of exact matches between the two aligned sequences in the HSP, dividing by the number of Query amino acids in the HSP and multiplying by 100. The polynucleotides of SEQ ID NO:X which encode the polypeptide sequence that generates an HSP are delineated by columns 8 and 9 of Table 2.

[055] The PFam database, PFam version 5.2, (Sonnhammer et al., Nucl. Acids Res., 26:320-322, (1998)) consists of a series of multiple sequence alignments; one alignment for each protein family. Each multiple sequence alignment is converted into a probability model called a Hidden Markov Model, or HMM, that represents the positionspecific variation among the sequences that make up the multiple sequence alignment (see, e.g., R. Durbin et al., Biological sequence analysis: probabilistic models of proteins and nucleic acids, Cambridge University Press, 1998 for the theory of HMMs). The program HMMER version 1.8 (Sean Eddy, Washington University in Saint Louis) was used to compare the predicted protein sequence for each Query sequence (SEQ ID NO:Y in Table 1A) to each of the HMMs derived from PFam version 5.2. A HMM derived from PFam version 5.2 was said to be a significant match to a polypeptide of the invention if the score returned by HMMER 1.8 was greater than 0.8 times the HMMER 1.8 score obtained with the most distantly related known member of that protein family. The description of the PFam family which shares a significant match with a polypeptide of the invention is listed in column 5 of Table 2, and the database accession number of the PFam hit is provided in column 6. Column 7 provides the score returned by HMMER version 1.8 for the alignment. Columns 8 and 9 delineate the polynucleotides of SEQ ID NO:X which encode the polypeptide sequence which shows a significant match to a PFam protein family.

[056] As mentioned, columns 8 and 9 in Table 2, "NT From" and "NT To", delineate the polynucleotides of "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFam/NR database as disclosed in the fifth column of Table 2. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the polynucleotides of SEQ ID NO:X delineated in columns 8 and 9 of Table 2. Also provided are polynucleotides encoding such proteins, and the complementary strand thereto.

The nucleotide sequence SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, the nucleotide sequences of SEQ ID NO:X are useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in Clone ID NO:Z. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to these polypeptides, or fragments thereof, and/or to the polypeptides encoded by the cDNA clones identified in, for example, Table 1A.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

[059] Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, and a predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing cDNA Clone ID NO:Z (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

[060] The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

RACE Protocol For Recovery of Full-Length Genes

Partial cDNA clones can be made full-length by utilizing the rapid [061] amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad. Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, SalI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or Sall, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., Nucleic Acids Res., 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

[063] An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

[064] Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., Nucleic Acids Res., 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be

used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase, if used, is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the immune/hematopoietic antigen of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant immune/hematopoietic antigen.

[065] The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as shown, for example, in Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEQ ID NO:X described, for example, in Table 1A (Clone ID NO:Z). A clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore, although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion

thereof) described in, for example Tables 1A or 2 by procedures hereinafter further described, and others apparent to those skilled in the art.

- [066] Also provided in Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.
- [067] Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128,256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into E. coli strain XL-1 Blue, also available from Stratagene.
- Vectors pSport1, pCMVSport 1.0, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus 15:59-* (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).
- [069] The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (Clone ID NO:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed

sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

- [070] Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of immune/hematopoietic associated genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by SEQ ID NO:X or the complement thereof, and/or the cDNA contained in Clone ID NO:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.
- [071] The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.
- [072] The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.
- [073] The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the immune/hematopoietic polypeptides of the present invention in methods which are well known in the art.

[074] The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence contained in Clone ID NO:Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, a polypeptide encoded by the cDNA contained in Clone ID NO:Z and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA contained in Clone ID NO:Z.

[075] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine. ten, or more of the complementary strand(s) of the sequences delineated in Table 1B column 6, or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B. column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic

acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[076] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

Further, representative examples of polynucleotides of the invention [077]comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[078] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the

invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. In preferred embodiments, the polynucleotides of the invention comprise, or alternatively consist of one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, wherein sequentially delineated sequences in the table (i.e. corresponding to those exons located closest to each other) are directly contiguous in a 5' to 3' orientation. In further embodiments, above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[079] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[080] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to

the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same Clone ID NO:Z. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

- In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same row of column 6 of Table 1B. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.
- [082] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.
- [083] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X are directly contiguous Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower

stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[085] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides, are also encompassed by the invention.

[086] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10

polynucleotides of another sequence in column 6 are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same Clone ID NO:Z (see Table 1B, column 1) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[088] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one sequence in column 6 corresponding to the same contig sequence identifer SEQ ID NO:X (see Table 1B, column 2) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[089] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of

one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same row are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[090] Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. Accordingly, for each contig sequence (SEQ ID NO:X) listed in the third column of Table 1A, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, b is an integer of 15 to the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. More specifically, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b; where a and b are integers as defined in columns 4 and 5, respectively, of Table 3. In specific embodiments, the polynucleotides of the invention do not consist of at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. as disclosed in column 6 of Table 3 (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for

example, the actual sequence contained in an identified BAC clone). In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by reference in their entirety.

TABLE 3

	Accession #'s	AI760827, AW408019, AI253155, AI349366, AI356482, AA814034, AW075920, AW407984, AI760691, AA251937, AI766650, AA352825, AA243541, AI934100, AA352840, H72208,	H/2106, AW193021, AL035530, AL035530, and AL035530. AL356513, AL356513, AL356513, AL358796, and AL358796.	AC006479, AC006479, AC006479, and AC006479.	AI240823, AC012580, AC012580, AC012580, AL133502, and AL133502.	AL133216, AC024998, AC024998, AL365438, AL365438, AL390122, AL390122, AL133216,	AL133216, AL133216, AC022/02, AC022/02, AC025/96, AC025/96, AF198096, AF198096, and AF198096.	AI908374.	AL117337, AF205588, AL022345, AL022345, AL022345, AL161931, AL161931, AL161931,	AL354975, AL354975, AL354975, AL355583, AL355583, AL355583, AL023808, AL023808, AFAGESO AFAGESO AFAGESO AT 117777 AT 117777	A 56.17815	AC021215		AI150061, AA382210, AC011448, and AC011448.	AI114447, AL133243, AL133243, AL133243, and AL133243.	AA312172.	AB023431, AC005954, AC005954, AC005954, and AC068475.		AA904376, H23157, AA663798, AA359944, AA448036, R61429, H09004, AA309011, AF126245, AP001785, and AP001785.	AI057188, AW273323, C15735, AI932257, AI028587, AI940493, AW043720, AW021811,	AA858079, AW197210, AI791278, AA508647, C15853, AA181800, AW043729, AW008982, A1018022, A1085340, A A031478, A A A 282785, A C007303, 782108, A I 031121, A I 121840	L24095, AC004882, AC005529, AC002070, AC008984, AL132985, AL049781, Z72006,	AC005881, AL079305, AP000263, AC005888, AC003080, AC004935, AL035667, AC005610,	AP000036, AC005186, AC004842, AL035696, AC003661, AC004503, AC009263, AL023581, AC003009 1141096 AL021368 AP000567 AC004933 AC003975 AP000494 AL02638	AF015262, AL049833, AL034350, AL031010, AJ229043, AP001069, AC006288, AL049561, AL074507 AC005701 AP000100 AC005792 AP000566 AL073283 AC011594 AC006377
aimer	Range of b	58	15 - 319 AI	6	-		All	15 - 567 AI		AI	15 451 A		-	15 - 399 AI	15 - 238 AI		15 - 233 AE	7	15 - 626 AA	15-389 AI	AA	12	ÀC	AP	AF
RST Disclaimer	Range of a	1 - 3744	1 - 305	1-375	1 - 849	1 - 89		1 - 553	1 - 587		1 - 437	1-415	1 - 274	1 - 385	1 - 224	1 - 657	1 - 219	1 - 713	1 - 612	1 - 375					
Contig	D:	961376	573692	526312	958768	521835		931477	964871		864366	573989	669802	503573	573993	932514	861018	922800	935414	614849					
SEQ ID	×	11	12	13	14	15		16	17		18	61	20	21		23		25	26	27					
Clone ID	NO: Z	НАМНВ21	HASAX16	HASAY74	HASAY89	HASAY94		HBCAL36	HBCAL39		HRCAM74	HBCAR79	HBCAS69	HBCAT17	HBCAT63	HBCBM52	HBCBX12	HBCBZ05	HBDAC79	HBDAD04			-		

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	1 - 519	1 - 369	1 - 422	1 - 426	1 - 390	1 - 452	1 - 435	1 - 357	1 - 414	1 - 384	1 - 589	1 - 415	1 - 375	1-917	1 - 403	1 - 561	1 - 233																
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					* /*/w/									HBJKC52				HBJKC56	HBJKC86	HBJKD68	HBJKE63	HBJKF06	HBJKF86	HBJKI26	HBJLB78	HBJLC51		HBJLD57	HBJLD73

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735748	864013	952791	656721	665874	847840																	•			_ -		-					•				
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	1 - 322	1 - 332	1 - 341	1 - 882	1 - 354	1 - 374		,	1 - 646	1 - 179	1 - 454	1 - 531	1 - 467			1 - 426	1 - 379
	734522	752810	657747	843811	779004	823400	•		661665	725095	726491	760155	975088			792110	675692
	183	184	185	186	187	188	• .		189	190	191	192	193		-	194	195
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			AW182540, AA610084, AI936489, AA306791, AW340569, AA905749, and AB033050.	AW004683, H87822, H87851, and AW015156.	AC004254.	AL031657.	AI241023, AW401921, and AB023483.	AC002368.	H55415, W22115, AL096701, and AB011114.		AA601336, AA640305, AW341878, AI567676, H79323, AA593168, AW020612, AA167656,	AW085626, AA729004, N27362, F35374, N49298, AA179364, W45416, AI520984, T89141,	R99617, AI253347, AI918661, AI061158, AI281622, AA947352, AA228268, AA664963, W27084,	AA761454, F01694, T57636, AA299490, AI744890, N63562, AI640905, AI919048, H81012,	AI569452, AA828840, AI828721, AA496042, AW028376, AI343808, AA776663, AA428991,	AI363336, AI149177, AL049743, AF165926, Z83840, AL109984, AL031311, AC005412,	AC004821, AC007686, AC007546, AC007207, U85195, AC005377, AC007421, AC008115,	U95742, AE000658, AC004832, AL035587, L78833, AC007216, AL020997, AL031589,	AC004797, AC005520, AL035420, AF196779, AF139813, Z98200, AL033392, AC003025,	AL035086, AL080243, AL121655, AC006530, AC005355, AC002312, AJ246003, AC004228,	AC004895, AC005180, AL096791, AC006312, AP000512, AC005519, AC006285, AC005081,	AL049869, Z82190, AC005839, AC005015, AL049694, AC004816, AC006071, AC005726,	AC002120, AL031293, AC005089, AC006121, AL021453, AC005527, AC005696, AC006139,	AL135744; AL133163, AF217403, Z97630, AC005971, AL035422, U78027, AC004878,	AC004975, Z82176, AF023268, AC000025, AL121603, AL008582, AL049757, AF001549,	AC005399, AC005914, AC007387, AC005207, AC000048, AF207550, AC005821, AC002094,	AP000248, AC005876, AC002117, AC005231, AC005288, AL034429, AC006130, AF111167,	AP000704, AL133448, AL096701, AC007386, AF111168, AC005529, AL031280, Z98884,	Z73979, AF134726, AC004099, AC006581, AF051976, AC006160, AC006077, Z93020,	AC004212, AL008734, AL031655, AC007993, AC005695, AP000555, AC004913, AC007308,	AF109907, Z97056, AC005277, AL020995, AC003041, Y18000, AL117329, AC007263,	AL034421, AP000503, AP000008, AC004967, AP000514, AC004834, AC002558, AL034420,	U52112, AC005632, AL022333, AC005755, AL049780, AL031123, AC007055, AL133246,	AC005911, AC005049, AC003109, AD000092, AC004897, AC007226, AC005183, AC005829,	AL023807, AL122020, AL109952, AD000864, and AC005993.	
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691179	720050	720047	935952	794129	614911	864004	760833	090669	576429	964484	740142									<u> </u>					•							,				726480
196	197	198	199	200	201	202	203	204	205	206	207								1	,										•						208
HBJMF30	HBJMF47	HBJMI76	HBJMK34	HBJMK94	HBJML28	HBJML69	HBJMM72	HBJMN75	HBJMQ86	HBJMR15	HBJMR60					,																				HBJMT52

	L	AI810024, AW023610, and AA609969.		AW166629, AA601349, AA052895, N66744, AI732437, AI114704, T86740, AA491447, T98482, AA918759, AA663115, AA663086, AA291630, H72049, AW084938, R11040, AI926873, AW440498, T87973, AA846969, H93001, N63743, AA603883, AW028174, AA838162, AA507035, AA706845, AA837385, AA291700, AA297496, H73336, AA352365, AC004961, AL133382, AL034411, Z73420, AC002352, AC004887, AC003108, AC004645, U91326, AC006111, AC005509, AC004081, AL008712, AC016831, AL031276, AL033392, AC005531, AC007298, AL080286, AC004950, AL020993, AF196969, AP000365, AL021939, AP000295, AP000044, AP000112, AP000152, AC004223, AC007663, AC006549, AF001549, AC003714, AC002544, AJ010770, AL031584, AL121595, AB014080, AF017104, AB026898, AL080312, AL034408, AF020662, AC000078, AL109798, Z95331, AC002400, AC006441, AC002365, Z85987, AF196779, AC007364, AC004167, AL034582, AC016027, M98447, U82671, AL099179, and AP000553.				AA985391, AI053911, AA548890, AW403888, AL037632, AA081462, AI470646, AA834809, AA5888001, AA833896, AA833875, AI580250, AA912287, AA483771, AA380354, H59372, AA588001, AA833896, AA580808, AW196064, H61630, AW301350, AL138096, AA515457, AI791913, AI792133, N54894, AI821714, AA679154, AI282511, AA483218, F25733, AI270096, AL119713, AL120687, AI283312, AA683258, AA507822, AA457642, AA491862, AA8338190, AA491650, AW270270, H70994, AI821785, AW440545, H69109, AC007226, AF003528, AL031905, AC005815, AL008715, AC005036, AC008055, Z98941, AL096772, AC023172, AC005144, AC006013, AC007435, AP000201, AP000093, AC007488, AP000088, AC005722, AC002480, AL049712, AC002523, AP000201, AP000093, AC005881, AC007447, Z82198, AP000097, AP000237, AF107258, AC007437, Z74739, Z86064, AI229042, AC005261, AC007298, AL023807, AC0042495, AC0050811, AL078459, AL0135089, AL079342, AL024495, AC005284, AC004741, AL121595, AC002499, AL021978, AC005874, AF134471, AC005146, U91323, U82668, AC002536, AP000966, AC007262, AL033379, AC004948, AL080239, AC002091, AC007681, AL049744, AC010200,
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1 - 469	1 - 643	1 - 338	1 - 353	1 - 347	1 - 382	1-516	1-341	1 - 767
952862	060699	614930	933143	690404	703843	809996	786707	576434
209	210	211	212	213	214	215	216	217
HBJMV72	HBJMW20	HBJMX04	HBJMX21	HBJMX29	HBJMX34	HBJNC11	HBJNC89	HBJND59

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	1 - 298	1 - 414	i - 348	1 - 560	1 - 632	1 - 325	1 - 341	1 - 289	1 - 199	1 - 407	1 - 362	1 - 453	1 - 461	1 - 533	1 - 355	1 - 349	1 - 179	-			,		. •	
	578887	573103	921417	506594	760737	578869	971172	732250	753141	935819	775670	496513	702457	689705	967111	863938	677240					•		
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	HBMBC18	HBMBC25	HBMBC35	HBMBC91	HBMBE72	HBMBE84	HBMBH36	HBMBH55	HBMBH91	· HBMBI06	HBMBN32	HBMB020	HBMBQ33	HBMBQ83	HBMBS11	HBMBT85	HBMBU24			,				

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				AW274355, AI250646, AW088899, AA176980, AI336582, AW167229, AI251221, AI349957,
		,		AW131952, AA653459, AI285439, AW161579, AI885949, AI582871, AI581033, AI224463,
				AL048644, AW274192, AI500706, N27632, AI254727, AI500662, AI471429, AW301505,
	٠			W48671, AI340511, AI624304, AA857847, AI679959, AI633061, AW022494, AI348870,
				AI571699, AI699154, AW020288, AI702527, AA420722, AI349814, AI349186, AI336575,
				AW020710, AW023859, AI609375, AI349772, AL038463, AW020397, AI334895, N63128,
				AA579232, AA635382, AW082835, AI815232, AI335476, AI343030, N33175, AI471909,
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		,	,	AW075382, AI859644, AA629977, R32821, AW020826, AA062896, AI927233, AI348895,
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			-	AL045626, AW151979, AI866469, AI865116, AI553669, AI252077, AI348897, AI250627,
				AW274318, AI500714, C16221, AI950892, AI633125, AL048499, N22276, AL047344,
	,			AL137562, AL137712, AR068466, E12579, AL117440, S77771, AR038854, AL133093,
				AF043642, A08913, L04504, U89295, A08912, X06146, E12580, AL133606, A08910, E01573,
		,		E02319, A18777, A08909, AL049324, X99257, X57084, U80742, S76508, AL137276, A08908,
-				S36676, AL122123, AL080074, A08907, L40363, AF090886, S69407, AL049452, AL110196,
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			t	AF150103, AR064250, AB019565, AJ131955, AL133636, AL050280, AB025103, AF079763,
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-				E03671, AF200416, AF017790, I30339, I30334, I48978, AL096720, AF090896, AL133565,
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			_	AF016271, E01614, E13364, U91329, AL137292, AJ012755, U72620, I89944, AF026816,
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		,		U75370, AF047443, AF032666, X72889, AL137550, AF001552, L24896, AF115410, U75932,
· · · · · ·				AF091084, AL133104, AF175903, AL117644, AR054987, Y11254, AF141289, AL137538,
				AL133557, AL133016, AF036268, U57352, AL080132, AL080137, Y10080, AL137548,

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				AA027081, AI525653, AI525669, AI557238, AI557808, AI557602, AI547225, AI557426,	AIS41321, AW020592, AW022727, AW021178, AIS41056, AW022874, AIS41048, AW020406, AW019988 AW021777 AW022826, AW022299 AIS57222, AIS5802, AW020405, AW022308	AW020328, AI886206, AW020634, AW023351, AW021693, AI557258, AW020931, AW022981.	AW021182, AW020480, AW021466, AW022593, AW020629, AW023884, AI525857,	AW021561, AW021059, AI525656, AW023617, AW020295, and AC007655.	AA677098, and AC004814.		F34605, AL046519, Al340151, N69399, Al246061, AA229159, F00350, Al302350, H64549,	F24745, R68706, H16875, AW071109, AI204309, AA523719, AA778580, AA456149, M85827,	AI280566, M78026, Z30049, W45215, AA648957, H68343, AC012384, AC002480, AC005531,	AL008710, AL035079, AL031729, AL049631, AC004025, AC004983, AL022320, U80017,	AC007488, AC004477, AL121769, AL022397, AP000300, AC002994, AL049832, AC002350,	AC007172, AC007066, AC006449, AP000113, AP000045, AC007014, AC004466, AC003681,	AC006557, AC004791, AL031054, AC007880, AF109907, Z98884, AC005529, AC004797,	AC002310, Z99943, AE000658, AC006101, AP000346, AL049712, AC003046, U15177,	AC004874, AC005516, AL022316, AC002990, Z83822, AP000354, AC007040, AC005527,	U91323, AC005191, Z82194, AL135745, AF001550, AC004656, AL031668, AC005829, Z95114,	AL021707, AL121653, AC004448, AL121852, AL021578, AC004890, AC005184, AC005486,	AC006141, AL008718, AC007228, AC004584, AC000003, AC003108, AC007919, AF196971,	AP000501, AL096711, AC004816, U96629, AC006120, AF207550, AL031655, AC004263,	AC005846, AC002367, AC006576, AL034429, AJ003147, AC007955, AC002369, AL049709,	Z86090, AL034420, AC018633, AL121748, AC000159, AL035420, AC006509, AC004953,	AC002528, AC004878, AC005015, AC005280, U89337, AC005049, AC002303, AC006137,	AC005099, AL008635, AC007546, AC005696, AC004858, U89335, AL035681, AC003029,	AF024533, AL031255, AC005664, AC005207, AL109984, AL035587, AC005865, AL022326,	AC005844, AC007182, AC005753, AC000097, AL008725, AL031848, AC006547, AC002470,	U91325, AC000379, AB015355, AC005164, U91318, AL035652, AC005332, AC002091,	AL049869, AC006468, AC005007, U95742, AC002565, AC006538, AC007707, AC005158,	AC005800, AL031733, AC003075, AC005037, Z85986, AC005859, AC007216, AL031643,	AC004223, Z84487, AB003151, AP000688, AL034423, AL022722, AC005736, AL031591,	AC003982, AF069291, AL034553, AC002312, Z82190, Y10196, AC004098, AC004967, AD000313, AC003050, AL035240, Z05704, AC005107, AC00543, AC005484, Z03, AD00543	AI 000313, AC003930, AL033247, L73 / 04, AC003171, AC007342, AC003404, and AR0300 / 2.
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924183	888206	750274	861576	739316					657382	952830	805554	٠			,									,			•					*******		,	
257	258	259	260	261					262	263	264													,										-	
HBMDC03	HBMDC16	HBMDC88	HBMDD36	HBMDD59					HBMDE19	HBMDF55	HBMDH79																								

		768097, AA937687,	58060, AA487858,	13972, AA501578,	654, AA582911,	50, AA602528,), R38154,), AA525824,	A678499, AA743978,	399, T05101, R89294,	435, AI270117,	4, AA113861,	05126, AI278997,	AA075995,	37677, AA632837,	, AA703887,	50, N66428,	VW438643,	11, AA233519,	86562, AI471481,	665021, AW419118,	21747, AA449088,	160, AA368936,	AI564185,	775940, AL044940,	86, AI801591,	7, AI918421,	049722, AI133636,	2, AI674873,	AA352803, R97969,	58736, AI287528,	302, AP000114,	, AF060568, M27161, \	.031447, AL035420,	- 1001000 1 4100
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		AW303196, AW274349, AW301350, AI754955, AA649722, AA634145, AA768097, AA937687,	AA810370, AA719080, AA573020, AA644207, AA709005, AA504638, AA558060, AA487858,	AA568778, AA649705, AA579736, AA554319, AA858197, AA461233, AA513972, AA501578,	AA814522, N29933, AA132914, AA483731, AA480790, AA824655, AA824654, AA582911,	AA077817, AA437161, AI830390, AA523815, AA350859, T15897, AA650450, AA602528,	AA670468, AA861959, R97934, AA845813, AI434706, AI962050, AI284640, R38154,	AA610493, AW440976, H50727, AI251002, AW236342, T07451, AA167659, AA525824,	AA577906, T71030, AA229785, AA522942, AA603156, R97326, T06828, AA678499, AA743978,	AA504871, AA578481, AA492140, AA623002, AA970213, AI625244, M77899, T05101, R89294,	AA199616, AA490183, AW193265, AI282832, F18974, AA259245, AW276435, AI270117,	AA826303, AI688846, AA605032, AA649642, AI824562, AA745104, T41124, AA113861,	AA720548, AA729721, AA634146, AA525876, AA326589, AA569167, AI205126, AI278997,	AA552885, H64778, AA346575, AA610611, T08438, AA325817, AI339850, AA075995,	AW029038, AA558015, AA947360, AA804379, AI929531, AA664015, AA837677, AA632837,	AA515435, AA550758, AA973803, AA483068, H63607, AA774184, F32800, AA703887,	AA719805, AI434695, T06556, AW088058, AI537955, AA177061, AA020850, N66428,	AA594145, AI469172, F19012, F36273, AA401022, AI216799, AA886584, AW438643	AA578391, AI281697, N33611, AA252263, AA837084, AA446657, AA947811, AA233519	AĄ780797, AA847128, AA771811, AA491762, AI291124, AA378580, AA586562, AI471481,	AW166815, AA890235, AA713815, AA745410, AW162049, AA515051, AA665021, AW419118,	AA323749, AI291268, AW276827, AI014358, AA503473, AA610783, AW021747, AA449088,	AI537030, AA599920, AA605274, H10994, AL046409, AW440836, AA743960, AA368936,	AI341548, AI679782, AA813902, W16581, AI904894, AA678443, H64563, AI564185	AA601499, AA485291, AA598586, AW193432, AA779040, AA346454, AA775940, AL044940,	AI917271, AA557879, AI281881, AI469003, AI287651, AA385100, AA557686, AI801591,	AI446464, AI286264, AW302450, AF150152, AA325699, AA441788, T40077, AI918421	T41155, AA225155, T67750, AA678772, AA827295, N63352, AI431303, AI049722, AI133636,	AI567674, N25296, AA501722, AI002834, AA558697, AA747480, AI053672, AI674873,	AA644551, AA551503, W47183, F03097, AI350211, AI890923, AA468131, AA352803, R97969,	AA552945, AA569387, AW338500, AL046457, AA513293, AI375710, AA458736, AI287528,	AA587604, AP000130, AP000208, AP000247, AP001046, AL096701, AP000302, AP000114,	AP000046, U13056, U07000, Z83822, U14694, Y12508, U14719, AC004606, AF060568, M27161,	AC005994, Z82208, AF003528, U89335, AL049869, AC006210, U14718, AL031447, AL035420,	4P000307 M87916 143392 AC006241 AC003084 1114687 783075 AL040842 AC004034
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					R70884, AA747757, F33037, AA722146, D51877, AA133332, AI571161, F17529, AI559304,
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	1 - 651	1 - 139	1 - 338	1 - 316	1 - 330	4			1 - 306	1 - 311	1 - 303	1 - 329	1 - 243	1 - 462	1 - 559	1 - 316	1 - 178	1 - 311	1 - 236	1 - 462			1 - 394	1 - 234	1 - 208	1 - 275	1 - 685	1 - 227	1 - 191	1 598
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	HBMTW58	HBMTX29	HBMTX84	HBMTY82	HBMUA62			1	HBMUD12	HBMUF60	HBMUG57	HBMUH62	HBMUJ84	HBMUK59	HBMUN30	HBMU010	HBMU012	HBMU090	HBMUP35	HBMUT83			HBMUV03	HBMUY32	HBMUZ96	HBMVA83	HBMVE14	HBMVI79	HBMVI94	HBMV002

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HCFAW03	343	.924532	1 - 330	15 - 344	AI952593, AA402934, and T24885.
HCFAY27	344	784950	1 - 254	15 - 268	AA680371, and T85563.
HCFAY33	345	576058	1-166	15 - 180	AC005969.
HCFBA96	346	853961	1 - 176	15 - 190	AI613235, AA903469, AA813305, F25776, AW071554, AW150820, AW194200, AI983597,
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HCFBB14	347	628542	1 - 255	15 - 24 /	AA223831.
HCFBD91	348	850449	1 - 141	15 - 155	AF172244, and Z74023.
HCFBF07	349	953506	1 - 286	15 - 300	
HCFBG82	350	870890	1 - 551	15 - 565	AI127475, AI871007, AA142876, AI523587, AI830621, AW134689, AI825831, AA773904,
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HCFBI39	351	576018	1 - 330	15 - 344	
HCFBI80	352	216669	1 - 466	15 - 480	
HCFBL08	353	959617	1 - 289	15 - 303	
HCFBN62	354	576126	1 - 628	15 - 642	AA553332, AA343810, AI354333, AA496309, AA745302, F01222, N70957, AA757869,

AA584597, AW277135, AA297698, AA532875, AI146266, AW249720, T30864, AA484256, AW084161, AA295874, AA295865, AA225358, T63747, AA167549, AA229842, AI866971	AL096766, AC005225, AL133163, AC003663, AP000501, AC004927, D87675, AC005237,	AC006285, AC005089, AL031587, AC005215, AF111168, AL031176, AL034429, AL109801,	AL121655, AC004821, U07561, AP000359, L78833, AP000555, AL133241, AL022323,	AC016025, Z95114, AL117258, AP000343, AC002432, AC004216, Z93017, AL031276,	AL0350/1, AL050302, AL049569, AP000263, AC002395, AC005483, AP000036, AL049692,	AC005387, AL096791, AP000088, AL133448, AC000397, AC005808, AC006315, AL022163,	AC002106, AR004690, AC006430, X87373, AC005358, AC004983, AC005621, AC009069,	AL096703, AC008150, AC005755, AC005102, Z98884, AC006211, U82757, AC005740,	AC006128, AC005527, AB016897, and AC004476.		AF031077, AF031076, AF031078, and AF030876.	}	AI028522, AI040333, and AI055988.	F19258, AI820743, AI003172, W60516, AI003743, AA551509, AL038785, AW104748, AI365988,	AA635417, AI205126, AI762575, AA229785, AI914706, AI350211, AA584749, AA557325,	AA483204, AI962050, AA340003, AI917271, AW265294, F29989, AW166815, AA077935,	AI358229, AI904894, AI567674, AW339687, AA856981, AI635272, AI815000, F28576,	AI474713, AA973575, AI569086, AW080134, AI038279, AW337985, AA515051, AI079910,	AI133636, AW130799, AI445436, AI890052, AI963786, AI929531, AL079645, AA482711,	AI469003, AI433187, AI890923, AW162049, AL042856, AI679782, AA713815, AA077817,	F31619, AA344959, AL119391, AA579184, AA077952, AL041368, AW440836, AA558269,	AW029038, AW118011, AW105538, AI625244, N99715, AL040913, AW088202, AA228329,	AI421213, AI471729, AI358343, AW003434, AI866807, AW264969, F36273, AL048144,	AI499094, AI051551, AW069807, AI049722, AI339850, AW193432, AI284640, AW074398,	AI149915, AA904218, AW406755, AL041412, AW088616, AI244254, AL120674, AA340960,	C06327, AA365587, AI064952, AW265197, AI608626, AL046746, AI547286, AA743956,	AI653515, AA228420, AI282907, AA837755, AA339076, H88666, AI251002, AW275664,	AI305766, AA639025, AA601270, AI053535, AA745410, AW338500, AI963720, AI761471,	AW327360, AI565873, AI468134, AA366035, AI922840, AI886060, AA078483, F31204,	AI341664, AA826032, AI590038, T12272, AA501344, T29180, W49488, AI610159, AA533138,	AI934307, AA516326, T55510, AW407220, AI720141, AA601218, AA381665, AA515128,	AA365144, AI286264, C05755, AI688846, AA658235, AA826303, R89296, W38648, AA580662,	AW131034, AI291047, AI935827, AI918421, N58729, AI886365, AI827234, AW151016,	AW023672, AI821776, AW157005, AW193265, AI028510, AI613280, AW103239, AW419118,	AA98/962, AA669961, AA843430, A163/38/, A1082310, AA133986, A1931889, A1931928,
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AA732212, AA659774, AA528441, AI061334, AI201R23, AA492244, AI807372, AI124660, W96042, AI312790, AI3103909, H38386, AI05486, AI053604, AI654592, AI805256, AI110688, AI312790, AI836582, AI403809, H38368, AI05464, AI0537134, AI190891, AI4897573, AA443666, AI355857, AI411481, AI890928, AI65476, AI0537134, AI890570, AI806870, AI87582, AIA13286, AI205646, AI87590, AI13296, AI3780, AI13236, AI20691, AI8826, AI205691, AA43786, AI13286, AI205648, AI205646, AI13264, AI20591, AI48879, AI213246, AI20591, AI3780, AI13292, AI206917,	823, AA492244, AI807372, AI124660, 1054246, A1336054, A1564589, A1802526	11, AI890928, AI053476, AI053774, 961, C06458, AI,046409, AI557323	960, AI879000, AA115968, AI926846,	88, AW264973, AW192199, F13749,	57, AI349874, AI284467, AI719014,	4814, AC005040, AL023574, AL049589,	3, AC005954, AC004651, AC004029,	1, AC007436, AF045448, AC002295,	5025, AC008372, AC004592, AP000358,	384, AC007320, S48196, X53795, Z77894,	0011, AF015102, AC004169, AF000363, 400 AC006518 AL121694 AC005696	3, AP000855, AL023803, AL022323,	3164, Z82203, AC005999, AL022576,	959, AL021878, Z98950, AC003003,	Z98744, AC004866, AC005399, AC007671,	132, AC005156, AC005207, AC005754,	496, AP000047, AP000115, AF064863,	1, AL035402, AF120990, AC006512,	3312, AC006221, AC003088, AC005661,	551. AC006480. AC007262. AC006374.	5249, AC007543, AC004382, AC004789,	3, AC003001, AF030876, AC007558,	281369, AC004741, AC004808, AL009177,	160, AC005610, AF015171, AF015167,	;, AC006048, AC005262, AC003030,	10/, ACU08134, AF004837, U12383, AC005525 AC003105 AC005786	AC006150, AC005048, AL031012.	1103, AC005913, AC000111, U07000,	.945, AC007065, AC005822, AC005084,	1055 AT 100865 ACOOD134 ACOOSA06
	AA732212, AA659774, AA528441, AI061334, AI291 N26042, AI312790, AI431303, AI039809, H13868, A	AI110688, AI368745, AA457639, AI355587, AI4714, AI890570. AI806850. AW276827. AI038990. AW323	AI590591, AA489775, AA443065, AI588856, AW32	AF177861, AL138265, AI863283, AI886176, AA364, AA225195 AW238016, AL135643, AA53561, AA6	AA148489; AA715606, F35659, AA747889, AA3645	AC005694, AC005527, AC005529, AC007687, AC00	AC004617, AR060472, U29953, AC005924, AL1097.	AL133246, Z97630, AC005225, AL133297, AC0064	AC007845, AC005177, AC006285, AC005772, AC01	AP000954, AP000561, AC002430, AF165926, AÇ007 VI 132802, AC005233, AI 021027, AC004506, AC00	AP000133, AP000211, AC000062, AL035977, AC004500, AC00 AP000133, AP000211, AC000062, AL035695, AL036	AL049836, AF029308, AC003104, AL031286, Z9302	AC005229, AF002991, AC006537, AC003048, AC00	AL033381, AC008126, AP000359, AC004186, AC00	1C007051, A39972, AC004806, U12580, AC002462,	AF196779, AC004019, AC005341, AL031709, AC00	XL121578, L13713, L13714, S75337, AP000305, Z73	298/54, AC005922, AL034549, AC006511, AC00204	XB002329, AL033544, AC005387, AL035450, AC00 E164343 AD00040 AD000102 AE043045 AC005	r. 104543, Ar 000049, Ar 000193, Ar 045943, AC005 C005099, AP000117, AP000352, AL021808, AC007	C007461, AC006241, AC005832, AC007319, AC00	F140763, Z47046, AC005574, AC008165, AF03107	L078644, U47924, S75201, AL022393, AC006373,	L021939, AL079295, AC022517, AC002487, AF013	1040850 AP015169, AC001528, AF015168, L8164, AC005263 AL006521 AC005	// AEVEN AEV	C006456, AF190465, AP000495, AL109618, Z8290	C005589, AC004861, AC002347, AL050343, AC00	AC004832, AC018767, AP001037, AC004816, AC004945, AC007065, AC005822, AC005084,	AC004168 AC004831 AL031121 AC000052 AC007055 AL109865 AC000134 AC005406
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	HCFBU01	HCFBU38	HCFBU84	HCFBU85	HCFBW13	0011011	HCFBY02	HCFCA31	HCFCB67													- 1										٠

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	15 - 404	15 - 290	15 - 445	15 - 410	15 - 396	15 - 281	15 - 193				· · ·												`.								,			
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	HCFCC57	HCFCC68	HCFCC94	HCFCD44	HCFCF47	HCFCH47	HCFCJ21																											

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	15 - 356	15 - 270	15 - 375	15 - 423	15 - 437	15 - 379	15 - 465	15 - 482	15 - 164	15 - 678																		•	15 - 574	15 - 312	15 - 489	15 - 143	15 - 350
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	576096	576081	576094	860925	260925	506251	299925	506250	953522	805822																			954213	933017	664132	772262	576446
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HCFNK43 425 973548 1-693 15-707 HCFNK43 426 576008 1-350 15-373				-	•		AA663074, AA522500, AI439393, AA630122, H43771, AA532875, AI271985, AI342183,
HCFNK43 425 973548 1-693 15-707 HCFNK43 426 576008 1-350 15-373						,	AI798407, AA441810, AA728939, AA715418, AA225358, AW157731, T07346, AW377893,
HCFNK43 425 973548 1 - 693 15 - 707 HCFNK43 426 426 62608 1 - 350 15 - 373							AA772704, AA513125, AA525807, R87275, AI271766, AI368732, AA715075, AI870453,
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HCFNK43 425 973548 1-693 15-707 HCFNO55 476 576008 1-350 15-373							AF196971, U62292, AC006965, Z98884, AL021578, AC007637, AL023284, AC005088,
HCFNK43 425 973548 1-693 15-707					,		AL117694, AC002511, AC005763, AL022238, AC005488, Z73900, AP000008, AC009516,
HCFNK43 425 973548 1-693 15-707						,	AC006146, AC003663, AC006486, AL078581, AF196970, AC004821, AL031255, U95741,
HCFNK43 425 973548 1-693 15-707							AF042484, AC004531, AC006111, AC005609, AC005874, AF134471, AL021977, AC002404,
HCFNK43 425 973548 1-693 15-707		•					AL050308, AP000030, AC004583, AC004223, AC003108, AC005920, AP000269, AL135960,
HCFNK43 425 973548 1-693 15-707							AJ131016, AC004228, AC003957, AF030453, AC005753, Z93930, U63721, AL080248,
HCFNK43 425 973548 1-693 15-707	15						AL035659, AC004687, AF111170, AL022312, D87675, AC004611, Z84469, AF207550,
425 973548 1 - 693 15 - 707 426 576008 1 - 350 15 - 373	71						AL117344, AC009802, AL008715, AC008055, AL035086, AC004098, AL049872, AL117258,
425 973548 1 - 693 15 - 707 426 576008 1 - 350 15 - 373	•						AC004805, AC002563, AC004644, Z82206, AC005102, AC005086, AC002477, AL031587,
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				1 - 390	1 - 54	1 - 302	1 - 223	1 - 417	1 - 314	1-217	1 - 218	1 - 280	1 - 334	1 - 240	1 - 279					
	•			927654	670941	738408	989656	706427	504395	916651	916621	574164	959492	6429289	574256		<u> </u>			
				437	438	439	440	441	442	443	444	445	446	447	448					
				HCFOP46	HCÜAA60	HCUAD58	HCUAE70	HCUAG89	HCUAG92	HCUAH15	нслан60	HCUAH70	HCUAI71	HCUAK23	HCUAK49		,	ն		